

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 08:28:24 ; Search time 17 Seconds
(without alignments)
1206.802 Million cell updates/sec

Title: US-09-997-514-422

Perfect score: 2067

Sequence: 1 MFCLKLLILLVLLDYSGL.....RNNLEKSGGMEKTKQAF 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	168	8.1	365	1 CXAR_HUMAN	P78310 homo sapien
2	146.5	7.1	246	1 MYPO_HETFR	P20938 heterodontu
3	146	7.1	365	1 CXAR_MOUSE	P97792 mus musculu
4	140.5	6.8	249	1 MYPO_CHICK	P37301 gallus gall
5	138.5	6.7	215	1 CIB2_HUMAN	O60339 homo sapien
6	137	6.6	215	1 EVAL_MOUSE	O70255 mus musculu
7	137	6.6	338	1 LAMP_MOUSE	Q13449 homo sapien
8	135	6.5	338	1 LAMP_RAT	O62813 rattus norv
9	133	6.4	686	1 IPL2_MOUSE	O9ers6 mus musculu
10	132	6.4	248	1 MYPO_HUMAN	P25189 homo sapien
11	131	6.3	219	1 MYPO_BOVIN	P10522 bos taurus
12	131	6.3	248	1 MYPO_MOUSE	P27573 mus musculu
13	130	6.3	248	1 MYPO_RAT	O69907 rattus norv
14	128.5	6.2	319	1 A33_HUMAN	Q9np60 h x-linked
15	128	6.2	686	1 IPL2_HUMAN	P54900 rattus norv
16	127.5	6.2	215	1 CIB2_RAT	O8spv8 pan troglod
17	127	6.1	316	1 FCQA_PANTR	Q10656 caenorhabdi
18	125.5	6.1	1040	1 EG15_CAEEL	Q63203 rattus norv
19	123.5	6.0	285	1 FCQ2_RAT	O96pq1 mus musculu
20	123.5	6.0	595	1 SILL_HUMAN	P35917 homo sapien
21	123.5	6.0	1363	1 VGR3_MOUSE	O98919 gallus gall
22	122.5	5.9	338	1 LAMP_CHICK	Q9slh0 pan troglod
23	120.5	5.8	597	1 SILL_PANTR	Q9nzn1 homo sapien
24	119	5.8	696	1 IPL1_HUMAN	P60029 pan troglod
25	119	5.8	696	1 IPL1_PANTR	P01833 homo sapien
26	119	5.8	764	1 PIGR_HUMAN	P12318 homo sapien
27	118.5	5.7	317	1 FCQA_HUMAN	P35916 homo sapien
28	118.5	5.7	1298	1 VGR3_HUMAN	P15364 drosophila
29	118	5.7	333	1 ANAL_DROME	P22648 schistocerc
30	118	5.7	898	1 PAS2_SCHAM	O60487 homo sapien
31	117.5	5.7	215	1 EVAL_HUMAN	P97797 m protein-t
32	116.5	5.6	513	1 SHS1_MOUSE	P59823 mus musculu
33	116	5.6	695	1 IPL1_MOUSE	

RESULT 1

CXAR_HUMAN

ID CXAR_HUMAN STANDARD; PRT; 365 AA.

AC P78310; O00694;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Cocksackievirus and adenovirus receptor precursor (Cocksackievirus B-

adenovirus receptor) (hCAR) (CVB3 binding protein).

GN CXADR OR CAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97190109; PubMed=9036860;

RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,

RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.,

RT "Isolation of a common receptor for Cocksackie B viruses and

RT adenoviruses 2 and 5.";

RL Science 275:1320-1323(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97250541; PubMed=9096397;

RA Tomko R.P., Xu R., Philipson L.;

RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C

RT adenoviruses and group B coxsackieviruses.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

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RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

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RN [4]

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RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

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RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

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RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

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RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

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RX MEDLINE=20008750; PubMed=10543405;

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RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

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RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

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RL Hum. Genet. 105:354-359(1999).

RN [4]

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RN [4]

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RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

RA Bowles N.E.;

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RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

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RX MEDLINE=20008750; PubMed=10543405;

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RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

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RN [4]

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RA Bowles N.E.;

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RT Cocksackievirus B-adenovirus receptor gene.";

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RN [4]

RP SEQUENCE FROM N.A.

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RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

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RL Hum. Genet. 105:354-359(1999).

RN [4]

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RA Bowles N.E.;

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RT Cocksackievirus B-adenovirus receptor gene.";

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RN [4]

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RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

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RL Hum. Genet. 105:354-359(1999).

RN [4]

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RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; Y07593; CAA68868.1; --
CC EMBL; U90716; AAC51234.1; --
CC EMBL; AF169366; AAF05908.1; --
CC EMBL; AF169360; AAF05908.1; JOINED.
CC EMBL; AF169361; AAF05908.1; JOINED.
CC EMBL; AF169363; AAF05908.1; JOINED.
CC EMBL; AF169363; AAF05908.1; JOINED.
CC EMBL; AF169364; AAF05908.1; JOINED.
CC EMBL; AF169364; AAF05908.1; JOINED.
CC EMBL; AF169365; AAF05908.1; --
CC EMBL; AF200465; AAF24344.1; --
CC EMBL; AF242865; AAG01088.1; --
CC EMBL; AF242862; AAG01088.1; JOINED.
CC EMBL; AF242864; AAG01088.1; JOINED.
CC EMBL; BC003684; AAH03684.1; --
CC EMBL; BC010536; AAH10536.1; --
CC PDB; 1EAJ; 13-JUL-01.
CC PDB; 1F5W; 08-NOV-00.
CC PDB; 1KAC; 24-NOV-99.
CC Genew; HGNC:2559; CXADR.
CC MIM; 602621; --
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003598; IG_c2.
CC Pfam; PF00047; ig; 2.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS50835; IG-LIKE; 2.
CC Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT TRANSMEM 238 258
FT DOMAIN 259 365
FT DOMAIN 20 134
FT DOMAIN 141 228
FT DOMAIN 41 120
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FB64 CRC64;
8.1%; Score 168; DB 1; Length 365;
Query Match

Query Match

Best Local Similarity 21.8%; Pred. No. 2e-06;
Matches 87; Conservative 65; Mismatches 148; Indels 100; Gaps 18;

QY 5 LKLLLPVLDYSLGLNDLNVSPPELTVH--VQDSALMGCVFQ-STEDKCIFKIDWTLSLP 61
DB 5 LCFVLLGVVDFA---RSLSIITPEEMIEKAKGETAYLPCKFTLSPEQGPDLIEWLISP 61
QY 62 GEHAKDEYVLYYYSNLSVPIGRF---QNRVHL-MGDILNCGSLLLQDVQADQGYICE 117
DB 62 ADNQKVDQVILYSGDKIVDDYDPLDKGRVHFTSNDLKSGDASINVTLQLSDIGTYOCK 121
QY 118 IRLKGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVF---QSTEVGHVTKVEMIFS 173
DB 122 V--KKAPGVANKIKHLVWL-VKPSGARCVXDSEIEIGDFKIKCPKESGLPLQYEW--- 175
QY 174 GRRAKEEIVFYYVHKLKRMSEVYSQSGWGHFQNRVNLVGDIFRNDGSGIMLQGVRESQGNYT 233
DB 176 -----QKLSDSQKMTSW-----LAEMTSSV-----ISVKNASSESYGTVS 211
QY 234 CSHLGLNVLFPKTTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIVIGVICATILLPLVLI 293
DB 212 CTVR--NRVSDQCLRLNVVP-----SNKAGLIAGAIIGTLALALIG 254
QY 294 LIVKKTGKNSVSNVTVLKNVTKTNPETKEKPCHEGCEGKHYSPIIREVIEEEP 353
DB 255 LII-FCC-----RKRREEKYKEVHHD-----IREDPV 282
QY 354 SEKSEATVMTMHPVMPVPSLRSDRNN--SLEKKSGGGMPTQ 391
DB 283 PPKSRTSTARSY-----IGNSHSLGSMSPSNMEGYSKTQ 317

RESULT 2
MYPO_HETFR STANDARD; PRT; 246 AA.

AC P20938;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Blasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OC NCBI_TaxID=7792;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=90040744; PubMed=247817;
RX Saavedra R.A., Fors L., Aebbersold R.H., Arden B., Horvath S.,
RA Sanders J., Hood L.;
RT "The myelin proteins of the shark brain are similar to the myelin proteins of the mammalian peripheral nervous system.";
RL J. Mol. Evol. 29:149-156(1989).
CC -1- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Found only in peripheral nervous system Schwann cells.
CC -1- PTM: N-GLYCAN IS SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Belongs to the myelin P0 protein family.
CC
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CC
CC ENBL; X16714; CAB37865.1; -.

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DR PIR; A32999; A32999.
DR HSSP; P06907; INEU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG v.
DR InterPro; IPR000920; Myelin_P0.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00568; MYELIN_P0; 1.
KW Myelin; Structural protein; Glycoprotein; Transmembrane;
KW Phosphorylation; Immunoglobulin domain; Signal.
FT SIGNAL 1 27 BY SIMILARITY.
FT CHAIN 28 246 MYELIN P0 PROTEIN.
FT DOMAIN 28 150 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 151 178 POTENTIAL.
FT DOMAIN 179 246 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 143 IG-LIKE V-TYPE.
FT DISULFID 48 125 POTENTIAL.
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (COMPLEX) (BY
FT SIMILARITY).
SQ SEQUENCE 246 AA; 27335 MW; A776A9ED9D430FA0 CRC64;

Query Match 7.1%; Score 146.5; DB 1; Length 246;
Best Local Similarity 26.0%; Pred. No. 7e-05;
Matches 44; Conservative 37; Mismatches 61; Indels 27; Gaps 6;

QY 147 VGLIQMCGVFQSTE-VKHHVTKVWIFSGRAKEEI-VFRIYHKLRMSVEYSQSGHFQN 204
Db 40 VGSVDVLYCGFWSNEYVSDLTLESRRFPDMSRDIISIFHYGN---GVPIEKWGQFRG 95

QY 205 RVNIVGDIIFRNDGSIIMLGVRSDGNGVTCISHLGNLVFKKTVLHVSPREPRLVTPAA 264
Db 96 RVEMVGWDISKHDSIVIRNLDYIDNGTFTCDVKNPPDVGVTSDDVHVVVD-----K 147

QY 265 LRPLVLGNQLVIIVGVICATILLPLVL-----IVKKTGKNSS 305
Db 148 IPPVGAG-----VVSgaiGTLGILLVGLYLFYIVRRRARSETS 191

RESULT 3
CXAR MOUSE
ID_CXAR_MOUSE STANDARD; PRT; 365 AA.
AC P97792; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DD 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cocksackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hung J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cocksackie B viruses and
RT adenoviruses 2 and 5.";
RL Science 275:1320-1323 (1997).
[3]
SEQUENCE FROM N.A.
RP STRAIN=C3H/NAI;
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "hCAR and mCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356 (1997).
[3]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=98080429; PubMed=9420240;
RX [3]

```



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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Epithelial V-like antigen 1 precursor.
GN EVAI OR EVA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RW [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAG-2; TISSUE=Thymus;
RA MEDLINE=98252857; PubMed=9585423;
RA Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,
RA Mariani M., Teesalu T., Consalez G.G., Grassi F.;
RT "Epithelial V-like antigen (EVA), a novel member of the immunoglobulin
superfamily, expressed in embryonic epithelia with a potential role as
homotypic adhesion molecule in thymus histogenesis." ;
RL J. Cell Biol. 141:1061-1071(1998).
CC -!- FUNCTION: Mediates homophilic cell-cell adhesion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Expressed in liver and gut, skin, and testis
or not in thymocytes, lymphocytes, macrophage or dendritic cells
or cell lines.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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or send an email to licensed@isb-sib.ch).
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DR EMBL; AF030454; AAC40128.1; .
DR HSSP; P06907; LNEU.
DR MGD; MG1:1289160; Eva.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR000920; Myelin_P0.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR00213; MYELINPO.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;
KW Signal.
FT SIGNAL          1      26      POTENTIAL.
FT CHAIN           27     215    EPITHELIAL V-LIKE ANTIGEN 1.
FT DOMAIN          27     154    EXTRACELLULAR (POTENTIAL).
FT TRANSMEM       155     175    POTENTIAL.
FT DOMAIN          176     215    CYTOPLASMIC (POTENTIAL).
FT DOMAIN          27     141    IG-LIKE V-TYPE.
FT DISULFID        47     123    BY SIMILARITY.
FT CARBOHYD        39     39     N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD       118     118    N-LINKED (GLCNAC. . ) (POTENTIAL).
SQ SEQUENCE        215 AA; 24162 MW; F6SE36787CE69D5 CRC64;
Query Match              6.6%; Score 137; DB 1; Length 215;
Best Local Similarity   27.1%; Pred. No. 0.00036;
Matches 57; Conservative 33; Mismatches 92; Indels 28; Gaps 9;
QY      8 ILLPVLLDYSLGNDLVNVPPELTIVHVGDSALMGCVFOSTEDKCIFK-----IDW 57
DB      8 LVLPULL--SLQLTA--CPTAEVEIYTSGALEAVNGTDVRLKCTFSFAFPVGDAVTW 63
QY      58 TLSPGEAKDEVLYYYNSLVPI-GRPNRVHLMDGLNCDSLLLODVQEAQGTYVIC 116
DB      64 NFRPDGGREGVFVYHHNPDPFRPMISRGKRVRWDGNGPERYDVSIILLKLQFDONGTYTC 123
QY      117 EIR----LKGSQVFVKXAVLVHLPL-BEPKELVHVGVGLIQMCGVFQSTEV--KHVIKVE 169
DB      124 QKNPPDDVDGLGTIRLSVV-HTVPFEIYFLAIVAISAACAAMTIIVTVVLFQHFRRKR 182
QY      170 WI-----PSGRRAKEETIVRYHYHKLRMSVE 194

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EMBL; U31554; AAA86120.1; -
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_c2.
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS00835; IG LIKE; 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
Repeat; Signal; Lipoprotein.
SIGNAL 1 28
CHAIN 29 315
LIMBIC SYSTEM-ASSOCIATED MEMBRANE
PROTEIN.
PROPEP 316 338
DOMAIN 29 122
DOMAIN 132 214
DOMAIN 219 304
DISULFID 53 111
DISULFID 153 197
DISULFID 239 290
CARBOHYD 40 40
CARBOHYD 66 66
CARBOHYD 136 136
CARBOHYD 148 148
CARBOHYD 279 279
CARBOHYD 287 287
CARBOHYD 300 300
CARBOHYD 315 315
LIPID 315 315
GPI-anchor amidated asparagine
(Potential).
SQ SEQUENCE 338 AA; 37324 MW; 0576AFDD68A39B86 CRC64;
Query Match 6.5%; Score 135; DB 1; Length 338;
Best Local Similarity 19.8%; Pred. No. 0.00095;
Matches 71; Conservative 55; Mismatches 123; Indels 110; Gaps 14;

4 PLKLLLPVLDVSLGN--DLNVSPPELVHVDGSLMGCVFQSTEDK-----CIF 53
13 PLVLLRLCLLPTGLPVRSDVDFNRGTDNITVRQDGTAILRCVVDKSKVWLNRSGLIF 72
54 --KIDWTLSPGEHAKDYLYYYNSLVPIGRFQNVHLMDGLCNDGSLLLQDVQEQADQ 111
73 AGDKWSLDPRVELEKHALEY-----SLRIQKVDVYDE 106
112 GTVICEIRLKGESQVFKKAVLHLVPE---EPKELMVHVGGLQMGCVFQSTEV-----K 163
107 GSYTCSVQTQHEPKTSQVLLVQVPPKISNIDSVTVNEGSNVLVCMANGREPVTWIR 166
164 HVTKEVWIFSGR-----RAKEELVFRYHKLMSVEY-----SQS 198
167 HLTPLGREFEGEBEYLEILGITREQSGKYEKAAEVSSADVQKVTVNVPPTTESKS 226
199 -----WGHFQNRVNLVG--DIFRNDG--SIMLQVRSDDG 230
227 NEATTGQASLKCEASAVPAPDFEWTRDDTRINSANGLEIKSTEGOSSLTVTNVTTEHYG 286
231 NYTCSIHLGNLVEKFTIVLHVSPEEPRTLVTPAALRPLVGGNQLVIVGIVCATILL 289
287 NYTC-----VAANKLGVTNAS-----LVLFPRQSVRG-INGSLSLAVPLWLAASLFLCL 334

RESULT 9
IPL2_MOUSE
ID IPL2_MOUSE
AC Q9ERS6; Q9ERS6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE X-linked interleukin-1 receptor accessory protein-like 2 precursor
DE (ILIRAPL-2 related protein) (TIGIR-1).
GN ILIRAPL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Liver;
RX MEDLINE=20459050; PubMed=10882729;
RA Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S.,
RT Sins J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=21472256; PubMed=11587848;
RA Ferrante M.I., Ghiani M., Bulfone A., Franco B.;
RT "ILIRAPL2 maps to Xq22 and is specifically expressed in the central
RT nervous system.";
RL Gene 275:217-221(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9ERS6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9ERS6-2; Sequence=VSP_008056, VSP_008057;
CC Note=may be due to an intron retention;
CC -1- TISSUE SPECIFICITY: Detected in fetal brain after day 12.5, in
CC particular in parts of the diencephalon and in the basal plate of
CC the spinal cord, in postnatal brain detected in cerebral cortex,
CC olfactory bulb, in the CA1 region of the hippocampus and in
CC Purkinje cells of the Xth cerebellar lobule.
CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).

EMBL; AF284437; AAG21371.1; -
EMBL; AJ277831; CAC10559.1; -
MGD; MGI:1913106; Ilirap12.
InterPro; IPR007110; IG-like.
InterPro; IPR003599; IG.
InterPro; IPR004075; IL1_receptor1.
InterPro; IPR004077; IL1_receptor1p.
InterPro; IPR000157; TIR.
Pfam; PF00047; ig; 3.
Pfam; PF01582; TIR; 1.
PRINTS; PR01539; INTERLEUKINR2.
PRINTS; PR01537; INTRLEUKINRIF.
SMART; SM00409; IG; 2.
SMART; SM00255; TIR; 1.
PROSITE; PS00835; IG LIKE; 3.
PROSITE; PS50104; TIR; 1.
Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
Glycoprotein; Alternative splicing.
SIGNAL 1 16
CHAIN 17 686
DOMAIN 17 354
TRANSMEM 355 375
X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY
PROTEIN-LIKE 2
EXTRACELLULAR (POTENTIAL).
POTENTIAL.

FT	DOMAIN	376	686	CYTOPLASMIC (POTENTIAL).
FT	FT	32	132	IG-LIKE C2-TYPE 1.
FT	DOMAIN	141	232	IG-LIKE C2-TYPE 2.
FT	DOMAIN	239	347	IG-LIKE C2-TYPE 3.
FT	DOMAIN	400	559	TIR.
FT	DISULFID	53	116	POTENTIAL.
FT	DISULFID	162	214	POTENTIAL.
FT	DISULFID	265	331	POTENTIAL.
FT	CARBOHYD	63	63	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	120	120	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBSPLIC	350	354	DLIYK -> GLIFS (in isoform 2).
FT	VARSPPLIC	355	686	/FTID=VSP_008056.
FT	VARSPPLIC			Missing (in isoform 2).
FT	VARSPPLIC			/FTID=VSP_008057.
FT	SEQUENCE	686 AA; 78797 MW; 36160D1CDE9B8264 CRC64;		
FT	SEQUENCE	6.4%; Score 133; DB 1; Length 686;		
FT	Best Local Similarity	20.4%; Pred. No. 0.0035;		
FT	Matches	78; Conservative 60; Mismatches 130; Indels 114; Gaps 18;		
Qy	38	ALMGCVFQSTEDKCIK-----IDWTL-----PGEHAKDEYVLY-----YS-- 75		
Db	8	ALVVCASVSTNLKMWKRNVDGDCIDMSVDLKTVMALAGEPVRVKCALFYIYRTNSMA 67		
Qy	76	NLSVPIGRFQNRVHLMGDILCN-----DGSLLQDVQVADQGTIYCEIRLKGESQVF 127		
Db	68	QSTGLRLWYRNKGLDEPIIFSEVRMSKEEDAIWFHSAEODSGFYTCVLR--NSTYCM 125		
Qy	128	KKAVLVHLVPEPKELMHVHGLQMGCVFOS-----TEVKNTKVEMI-----FSGR 176		
Db	126	KVMSLSLTAENE-----SGLCYNSRIRYLEKSVTRKKEISCPDMDDFKSD 172		
Qy	177	AKEEIVERYHKLMSVVEYSQSGHGFQNRVNLVGDIFRNDGSIHQGVRESDGNGNYTCGI 236		
Db	173	QEPDVVVYKCKPKM-----WRSI-----IIOGNALLIQVQVEDGNGNYTCGL 216		
Qy	237	HLGNLVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVII-----VGIVCATILL 289		
Db	217	KVEGLVRRTELKVT-----ALLTDKPKPLFPMENQPSVIDVLQGLPLNIPCKAFPGF 271		
Qy	290	-----PVL-----ILIVKTCGNKSSVNSVLVKNVKNKTNPKE 324		
Db	272	SGESGPMYWMKGEKIFELAGHIREGEIRLLKHELGK-EVELTLIFDSV--VEADLAN 328		
Qy	325	KPCERCEGEKHIYSPPIVRE 346		
Db	329	YTCVENENGRKH--ASVLLRK 348		
RESULT 10				
MYPO HUMAN	STANDARD;	PRT; 248 AA.		
AC	P25189; Q16072; Q92677; Q9B667;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral			
DE	protein) (MEP).			
GN	MPZ.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=92062068; PubMed=1719967;			
RA	Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,			
RA	Uyemura K.;			
RT	"Isolation and sequence determination of cDNA encoding the major			
RT	structural protein of human peripheral myelin.";			

RL	Biochem. Biophys. Res. Commun. 180:515-518 (1991).
RN	[2]
RN	SEQUENCE FROM N.A., AND VARIANT CMT1B HIS-98.
RC	TISSUE=Spinal cord;
RX	MEDLINE=93356807; PubMed=7688964;
RA	Hayasaka K., Ohnishi A., Takada G., Fukushima Y., Murai Y.;
RT	"Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
RT	type 1.";
RL	Biochem. Biophys. Res. Commun. 194:1317-1322 (1993).
RN	[3]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=94154677; PubMed=7509228;
RA	Pham-Dinh D., Fourbil Y., Blanquet F., Mattei M.-G., Roessel N.,
RA	Latour P., Chazot G., Vandenbergh A., Dautigny A.;
RT	"The major peripheral myelin protein zero gene: structure and
RT	localization in the cluster of P0 gamma receptor genes on human
RT	chromosome 1q21.3-q23.";
RT	Hum. Mol. Genet. 2:2051-2054 (1993).
RN	[4]
RN	SEQUENCE FROM N.A.
RA	Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA	Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA	Phelan M., Farmer A.;
RT	"Cloning of human full-length CDSs in BD Creator(TM) system donor
RT	vector.";
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN	[5]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Skin;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalobio D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[6]
RN	SEQUENCE OF 24-248 FROM N.A.
RP	Nelis E., Timmerman V., De Jonghe P., Muylle L., Martin J.-J.,
RA	Van Broeckhoven C.;
RT	"Linkage and mutation analysis in an extended family with Charcot-
RT	Marie-Tooth disease type 1B.";
RL	Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN	[7]
RN	REVIEW ON CMT1B VARIANTS.
RX	MEDLINE=95282670; PubMed=7762451;
RA	Roa B.B., Lupsaki J.R.;
RT	"Molecular Genetics of Charcot-Marie-Tooth neuropathy.";
RL	Adv. Hum. Genet. 22:117-152 (1994).
RN	[8]
RN	REVIEW ON CMT1B VARIANTS.
RX	MEDLINE=94302675; PubMed=7518101;
RA	Patel P.I., Lupsaki J.R.;
RT	"Charcot-Marie-Tooth disease: a new paradigm for the mechanism of
RT	inherited disease.";
RL	Trends Genet. 10:128-133 (1994).
RN	[9]
RN	REVIEW ON CMT1B AND DSS VARIANTS.
RX	MEDLINE=99103460; PubMed=9888385;

RA Nelis E., Haïtes N., van Broeckhoven C.;
RT "Mutations in the peripheral myelin genes and associated genes in
RT inherited peripheral neuropathies."; Hum. Mutat. 13:11-28(1999).
RL [10]
RL VARIANT CMT1B MET-30.
RP MEDLINE=94061030; PubMed=7694726;
RX Hayasaka K., Takada G., Ionasescu V.V.;
RA "Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
RT type 1B."; Hum. Mol. Genet. 2:1369-1372(1993).
RL [11]
RL VARIANT CMT1B CYS-82.
RP MEDLINE=94083941; PubMed=7505151;
RX Himoro M., Yoshikawa H., Matsui T., Mitsui Y., Takahashi M.,
RA Kaido M., Nishimura T., Sawaiishi Y., Takada G., Hayasaka K.;
RA "New mutation of the myelin P0 gene in a pedigree of
RT Charcot-Marie-Tooth neuropathy I."; Biochem. Mol. Biol. Int. 31:169-173(1993).
RL [12]
RL VARIANTS CMT1B GLU-90 AND GLU-96.
RP MEDLINE=94035113; PubMed=7693129;
RX Hayasaka K., Himoro M., Sato W., Takada G., Uyemura K., Shimizu N.,
RA Bird T.D., Conneally P.M., Chance P.F.;
RA "Charcot-Marie-Tooth neuropathy type 1B is associated with mutations
RT of the myelin P0 gene."; Nat. Genet. 5:31-34(1993).
RL [13]
RL VARIANT CMT1B SER-63 DEL.
RP MEDLINE=94035114; PubMed=7693130;
RX Kulkens T., Bolhuis P.A., Wolterman R.A., Kemp S., Te Nijenhuis S.,
RA Valentijn L.J., Hensels G.W., Jennekens F.G., de Visser M.,
RA Hoogendijk J.E., Baas F.;
RT "Deletion of the serine 34 codon from the major peripheral myelin
RT protein P0 gene in Charcot-Marie-Tooth disease type 1B."; Nat. Genet. 5:35-39(1993).
RL [14]
RL VARIANT CMT1B GLU-96.
RP MEDLINE=94068501; PubMed=7504284;
RX Su Y., Brooks D.G., Li L., Lepert J., Trofatter J.A., Ravetch J.V.,
RA Lebo R.V.;
RA "Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B
RT patients"; Proc. Natl. Acad. Sci. U.S.A. 90:10856-10860(1993).
RL [15]
RL VARIANTS DSS CYS-63 AND ARG-167.
RX MEDLINE=94100981; PubMed=7506095;
RX Hayasaka K., Himoro M., Sawaiishi Y., Nanao K., Takahashi T.,
RA Takada G., Nicholson G.A., Ouvrier R.A., Tachi N.;
RA "De novo mutation of the myelin P0 gene in Dejerine-Sottas disease
RT (hereditary motor and sensory neuropathy type III)."; Nat. Genet. 5:266-268(1993).
RL [16]
RL VARIANTS CMT1B LEU-78 AND ASN-134.
RP MEDLINE=95080774; PubMed=7527371;
RX Nelis E., Timmerman V., de Jonghe P., Vandenbergh A., Pham-Dinh D.,
RA Dautigny A., Martin J.-J., van Broeckhoven C.;
RA "Rapid screening of myelin genes in CMT1 patients by SSCP analysis:
RT identification of new mutations and polymorphisms in the P0 gene."; Hum. Genet. 94:653-657(1994).
RL [17]
RL VARIANT CMT1B PHE-63.
RP MEDLINE=96432254; PubMed=8835320;
RX Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P.,
RA Bonnebouche C., Corbillion E., Chazot G., Vandenbergh A.;
RA "Charcot-Marie-Tooth type 1B neuropathy: third mutation of serine 63
RT codon in the major peripheral myelin glycoprotein P0 gene."; Clin. Genet. 48:281-283(1995).
RL [18]
RL VARIANTS CMT1B LEU-78 AND CYS-101.
RP MEDLINE=96055517; PubMed=7550231;
RX Latour P., Blanquet F., Nelis E., Bonnebouche C., Chapon F.,
RA Diraison P., Ollagnon E., Dautigny A., Pham-Dinh D., Chazot G.,

Boucherat M., van Broeckhoven C., Vandenbergh A.;
 "Mutations in the myelin protein zero gene associated with
 Charcot-Marie-Tooth disease type 1B.";
 Hum. Mutat. 6:50-54(1995).
 [19]
 RN VARIANT DSS PHE-64 DEL.
 RX MEDLINE=96212920; PubMed=8630052;
 RA Ikedami T., Nicholson G.A., Ikeda H., Ishida A., Johnston H., Wise G.,
 ROuvrier R.A., Hayasaka K.;
 RT "A novel homozygous mutation of the myelin Po gene producing
 RJDejerine-Sottas disease (hereditary motor and sensory neuropathy
 RL type III).";
 RN Biochem. Biophys. Res. Commun. 222:107-110(1996).
 [20]
 RN VARIANT CMT1B SER-122.
 RX MEDLINE=97001227; PubMed=8844219;
 RA Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P.,
 ROuvrier R.A., Warner L.E., Garcia C.A., Russo D., Lovelace R.,
 RT Chance P.F., Lupeki J.R.;
 RJ "Myelin protein zero (MPZ) gene mutations in nonduplication type 1
 RL Charcot-Marie-Tooth disease.";
 RN Hum. Mutat. 7:36-45(1996).
 [21]
 RN VARIANT CMT1B SER-122.
 RX MEDLINE=97001227; PubMed=8844219;
 RA Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P.,
 ROuvrier R.A., Warner L.E., Garcia C.A., Russo D., Lovelace R.,
 RT Chance P.F., Lupeki J.R.;
 RJ "Myelin protein zero (MPZ) gene mutations in nonduplication type 1
 RL Charcot-Marie-Tooth disease.";
 RN Hum. Mutat. 7:36-45(1996).
 [22]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [23]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [24]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [25]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [26]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
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 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [27]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [28]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [29]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [30]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [31]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [32]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [33]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [34]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [35]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [36]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [37]
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 RX MEDLINE=96390490; PubMed=8797476;
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 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [38]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RL Hum. Mutat. 8:185-186(1996).
 [39]
 RN VARIANT CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
 RX MEDLINE=96390490; PubMed=8797476;
 RA Gabriels-Festen A.A.W.M., Hooogendijk J.E., Meijerink P.H.,
 RO Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kulkens T., Nelis E.,
 RT Jennekens F.G., de Visser M., van Engelen

RESULT 11	MYPO_BOVIN
ID	MYPO
AC	P1052
DT	01-JUN
DT	01-JUN
DT	10-OCT
DE	Myelin
DE	(MPP)
GN	MPZ.
OS	Bos t
OC	Eukary
OC	Mamma
OC	Bovide
OX	NCBI_
RN	[1]
RP	SEQUEN
RC	TISSUE
RX	MEDLIN
PA	Sakam

RT "Complete amino acid sequence of P0 protein in bovine peripheral
RT nerve myelin";
RL J. Biol. Chem. 262:4208-4214(1987).
CC -!- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -!- PTM: N-GLYCOSYLATION IS SULFATED.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Belongs to the myelin P0 protein family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M62860; AAA39867.1; -.
CC EMBL; M62857; AAA39867.1; JOINED.
CC EMBL; M62858; AAA39867.1; JOINED.
CC EMBL; M62859; AAA39867.1; JOINED.
CC HSSP; P06907; INEU.
CC MGD; MGI:103177; Mgz.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig v.
CC InterPro; IPR000920; Myelin_P0.
CC PRINTS; PR00213; MYELINP0.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG-LIKE; 1.
CC PROSITE; PS00568; MYELIN_P0; 1.
CC Myelin; Structural protein; Glycoprotein; Transmembrane;
CC Phosphorylation; Immunoglobulin domain; Signal.
CC SIGNAL 1 29
CC CHAIN 30 248 MYELIN P0 PROTEIN
CC DOMAIN 154 179 EXTRACELLULAR (BY SIMILARITY).
CC TRANSMEM 180 248 BY SIMILARITY.
CC DOMAIN 30 143 CYTOPLASMIC (BY SIMILARITY).
CC DOMAIN 50 127 IG-LIKE V-TYPE.
CC DISULFID 122 122 POTENTIAL.
CC CARBOHYD 122 122 N-LINKED (GLCNAC...) (COMPLEX).
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CC Query Match 6.3%; Score 131; DB 1; Length 248;
CC Best Local Similarity 25.4%; Pred. No. 0.0014;
CC Matches 45; Conservative 32; Mismatches 80; Indels 20; Gaps 6;
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CC QY 124 SQVFKAVLHLPEEPKELMHVHGLIQMCCVFQSTE-VKHVTKVVEIFSGRRAKEIV 182
CC Db 21 SLVLSPALAIIVVYTD--REIYGAVGSGQVTLHCSPWSEWSDDISFTWRYQPEGRDAIS 78
CC
CC QY 183 FRYVYKLRMSVEYSQSGHGFONRVNLVGDIFRNDGSIIMQGVRESGNGNYTCSIHGLNIV 242
CC Db 79 IFHYAK---GQPYIDEVGAFAKERIQWGDPRKDGSIIVHNLVDYSDNGTFTCDVKNPDI 135
CC
CC QY 243 FKKT--IVLHVSPEEPRTLVTFAALRPLVLGNQNLVIIVGIVCATILLPVLIVK 297
CC Db 136 VGKTSQVTLVFEKVPTRY-----GVVLGA-----VIGGLGVLLLLLFYLIR 180
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CC RESULT 13
CC MYPO RAT
CC ID MYPO RAT STANDARD; PRT; 248 AA.
CC AC P06507;
CC DT 01-JAN-1998 (Rel. 06, Created)
CC DT 01-JAN-1998 (Rel. 06, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
CC DE protein) (MPP).
CC GN MPZ OR P0.
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RT "Complete amino acid sequence of P0 protein in bovine peripheral
RT nerve myelin";
RL J. Biol. Chem. 262:4208-4214(1987).
CC -!- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -!- PTM: N-GLYCOSYLATION IS SULFATED.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Belongs to the myelin P0 protein family.
CC
CC PIR; A29128; A29128.
CC HSSP; P06907; INEU.
CC GlycoSuiteDB; P10522; -.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig v.
CC InterPro; IPR000920; Myelin_P0.
CC PRINTS; PR00213; MYELINP0.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG-LIKE; 1.
CC PROSITE; PS00568; MYELIN_P0; 1.
CC Myelin; Structural protein; Glycoprotein; Transmembrane;
CC Phosphorylation; Immunoglobulin domain.
CC DOMAIN 1 124 EXTRACELLULAR.
CC TRANSMEM 125 150
CC DOMAIN 151 219
CC DOMAIN 1 114
CC DOMAIN 21 98
CC DISULFID 93 93
CC CARBOHYD 93 93
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CC MOD RES 214 214
CC SEQUENCE 219 AA; 24710 MW; E4A882C1B7225FAP CRC64;
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CC Query Match 6.3%; Score 131; DB 1; Length 219;
CC Best Local Similarity 26.2%; Pred. No. 0.0011;
CC Matches 42; Conservative 27; Mismatches 73; Indels 18; Gaps 5;
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CC QY 141 KELMHVHGLIQMCCVFQSTE-VKHVTKVVEIFSGRRAKEIVFYVYHKLMSVEYSQSW 199
CC Db 7 KEVHGAVGSGQVTLVCSFWSSEWSDLSFTWRYQPEGRDAISIFHYAK---GQPYIDEV 63
CC
CC QY 200 GHFQNRVNLVGDIFRNDGSIIMQGVRESGNGNYTCSIHGLNIVFKKT--IVLHVSPEEP 257
CC Db 64 GTFKRIQWGDPRKDGSIIVHNLVDYSDNGTFTCDVKNPDIIVGKTSQVTLVFEKVPET 123
CC
CC QY 258 TLVTPAALRPLVLGNQNLVIIVGIVCATILLPVLIVK 297
CC Db 124 RY-----GVVLGA-----VIGGLGVLLALLLFYLIR 151
CC
CC RESULT 12
CC MYPO MOUSE
CC ID MYPO MOUSE STANDARD; PRT; 248 AA.
CC AC P21573;
CC DT 01-AUG-1992 (Rel. 23, Created)
CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
CC DE protein) (MPP).
CC GN MPZ OR P0.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91244320; PubMed=1709914;
CC RA You K.H., Hsieh C.L., Hayes C., Stahl N., Francke U., Popko B.;
CC RT "DNA sequence, genomic organization, and chromosomal localization of
CC RT the mouse peripheral myelin protein zero gene: identification of
CC RT polymorphic alleles";

OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85124601; PubMed=2578885;
 RA Lemke G., Axel R.;
 RT "Isolation and sequence of a cDNA encoding the major structural
 RL protein of peripheral myelin."
 RL Cell 40:501-508(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90166482; PubMed=2483091;
 RA Lemke G., Lamar E., Patterson J.;
 RT "Isolation and analysis of the gene encoding peripheral myelin
 RL protein zero."
 RL Neuron 1:73-83(1988).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 30-148.
 RX MEDLINE=96413553; PubMed=8816707;
 RA Shapiro L., Doyle J.P., Hensley P., Colman D.R., Hendrickson W.A.;
 RT "Crystal structure of the extracellular domain from P0, the major
 RL structural protein of peripheral nerve myelin."
 RL Neuron 17:435-449(1996).
 CC -i- FUNCTION: Creation of an extracellular membrane face which guides
 CC the wrapping process and ultimately compacts adjacent lamellae.
 CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -i- TISSUE SPECIFICITY: Found only in peripheral nervous system
 CC Schwann cells.
 CC -i- PTM: N-LINKED GLYCAN IS SULFATED.
 CC -i- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -i- SIMILARITY: Belongs to the myelin P0 protein family.
 CC -----
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 CC -----
 DR EMBL; K03242; AAA41576.1; -
 DR PIR; JQ0622; MPRT0.
 DR PDB; 1NEU; 15-MAY-97.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig v.
 DR InterPro; IPR000920; Myelin_P0.
 DR PRINTS; PR00213; MYELINP0.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 DR PROSITE; PS00568; MYELIN_P0; 1.
 KW Myelin; Structural protein; Glycoprotein; Transmembrane;
 KW Phosphorylation; Immunoglobulin domain; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 248 MYELIN P0 PROTEIN.
 FT DOMAIN 30 153 EXTRACELLULAR.
 FT TRANSMEM 154 179
 FT DOMAIN 180 248
 FT CYTOPLASMIC.
 FT DOMAIN 30 143 IG-LIKE V-TYPE.
 FT DISULFID 50 127
 FT CARBOHYD 122 122 N-LINKED (GLCNAC...) (COMPLEX).
 FT CONFLICT 43 43 G -> R (IN REF. 1).
 FT STRAND 31 33
 FT STRAND 37 41
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 FT STRAND 46 48
 FT STRAND 51 53
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 FT STRAND 77 83
 FT TURN 84 85
 FT STRAND 86 89
 FT TURN 94 97
 FT STRAND 99 101
 FT STRAND 104 104

FT HELIX 105 107
 FT TURN 108 108
 FT STRAND 109 109
 FT STRAND 112 114
 FT HELIX 119 121
 FT STRAND 123 130
 FT STRAND 138 147
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 Query Match 6.3%; Score 130; DB 1; Length 248;
 Best Local Similarity 25.1%; Pred. No. 0.0016;
 Matches 43; Conservative 32; Mismatches 74; Indels 22; Gaps 6;
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 DQ 29 AIVVYT-----DREYVGAVGSGQVTLHCSFWSSEWSDDISFTWRQPSGGRDAISIFHYAK 84
 QY 189 LRMSVEYSQSGHGFONRVNLVGDIFRNDGSIIMIQGVRESGNGNYTCSIHGLNLFVKKT-- 246
 DQ 85 ---GQPYIDEVGTGFKERIQWVGDPKWDGSIIVHNLDSYDNGTFTCDVKNPPDIVGKTSQ 141
 QY 247 IVLHVSPEEPTLVTPLALRPLVGLGNQLVIIVGIVCATILLPVLILIVK 297
 DQ 142 VTLVVEKVPTRY-----GVVIGA-----VIGGILGVVLLLLLLFYLIIR 180
 RESULT 14
 A33 HUMAN
 ID A33 HUMAN STANDARD; PRT; 319 AA.
 AC Q99795;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cell surface A33 antigen precursor (Glycoprotein A33).
 GN GPA33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=97165045; PubMed=9012807;
 RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
 RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
 RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
 RA Burgess A.W.;
 RT "The human A33 antigen is a transmembrane glycoprotein and a novel
 RT member of the immunoglobulin superfamily."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
 RN [2]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=97396159; PubMed=9245713;
 RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
 RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
 RA Simpson R.J.;
 RT "Characterization of posttranslational modifications of human A33
 RT antigen, a novel palmitoylated surface glycoprotein of human
 RL gastrointestinal epithelium."
 RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
 CC -i- FUNCTION: May play a role in cell-cell recognition and signaling.
 CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -i- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
 CC epithelium and in 95% of colon cancers.
 CC -i- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
 CC CARBOHYDRATE.
 CC -i- PTM: Palmitoylated.
 CC -i- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -i- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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Search completed: March 15, 2004, 08:34:38
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: March 15, 2004, 08:31:44 ; Search time 45 Seconds
(without alignments)
2762.537 Million cell updates/sec

Title: US-09-997-514-422

Perfect score: 2067

Sequence: 1 MFCPLKLLPVLDDYSLG.....RNNLEKKGGMPTQQAF 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_ivirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2067	100.0	394	4	Q86YT9
2	1985	96.0	384	4	Q8N9I7
3	1783	86.3	394	4	Q7Z499
4	1364	66.0	283	4	Q8NF70
5	982	47.5	379	11	Q8OUL9
6	198	9.6	335	13	Q9GV5
7	192	9.3	335	13	Q9PWR4
8	191	9.2	335	13	Q9YGH1
9	183	8.9	365	6	Q8WNV3
10	168	8.1	344	4	Q9UKV4
11	167	8.1	2828	4	Q9NR99
12	164	7.9	319	6	Q9TU80
13	158	7.6	373	4	Q9H6B4
14	154.5	7.5	373	11	Q920S5
15	152.5	7.4	372	11	Q8K1G0
16	152	7.4	319	6	Q9TU79

17	151.5	7.3	437	13	Q90WI4	Q90WI4 gallus gall
18	151	7.3	372	13	Q90Y50	Q90Y50 brachydanio
19	150.5	7.3	373	11	Q8R373	Q8R373 mus musculus
20	147.5	7.1	243	4	Q9UEL4	Q9UEL4 homo sapien
21	147.5	7.1	269	4	Q95297	Q95297 homo sapien
22	147	7.1	330	11	P97269	P97269 cavia porce
23	147	7.1	344	11	Q9R067	Q9R067 rattus norv
24	147	7.1	358	11	Q9R066	Q9R066 rattus norv
25	147	7.1	584	4	Q9Y3Y8	Q9Y3Y8 homo sapien
26	146	7.1	352	11	Q91W66	Q91W66 mus musculus
27	146	7.1	365	11	Q9DBJ8	Q9DBJ8 mus musculus
28	144.5	7.0	183	4	Q9UEL6	Q9UEL6 homo sapien
29	144.5	7.0	209	4	Q9NYK4	Q9NYK4 homo sapien
30	142.5	6.9	202	4	Q8IX11	Q8IX11 homo sapien
31	142	6.9	337	11	P97268	P97268 cavia porce
32	140	6.8	215	11	Q91WI4	Q91WI4 mus musculus
33	139.5	6.7	329	13	Q91AY6	Q91AY6 spherooides
34	138.5	6.7	318	13	Q91664	Q91664 xenopus lae
35	137.5	6.7	907	5	Q9NEG0	Q9NEG0 drosophila
36	137.5	6.7	3215	5	Q8IRV7	Q8IRV7 drosophila
37	137.5	6.7	4117	5	Q8IRV9	Q8IRV9 drosophila
38	137.5	6.7	4179	5	Q9W4V4	Q9W4V4 drosophila
39	137.5	6.7	4223	5	Q8MEN3	Q8MEN3 drosophila
40	137.5	6.7	4228	5	Q8IRV8	Q8IRV8 drosophila
41	136	6.6	338	4	Q8IV49	Q8IV49 homo sapien
42	136	6.6	339	13	Q9IAZ1	Q9IAZ1 spherooides
43	135.5	6.6	199	13	Q8JG36	Q8JG36 brachydanio
44	134.5	6.5	403	6	Q9N2H5	Q9N2H5 equus cabal
45	134	6.5	252	4	Q8WWT6	Q8WWT6 homo sapien

ALIGNMENTS

RESULT 1

Q86YT9 PRELIMINARY; PRT; 394 AA.

AC Q86YT9; 01-JUN-2003 (TREMREL. 24, Created)

DT 01-JUN-2003 (TREMREL. 24, Last sequence update)

DT 01-OCT-2003 (TREMREL. 25, Last annotation update)

DE Adhesion molecule AMICA.

GN AMICA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1] _

RP SEQUENCE FROM N.A.

RA Foster J.S., Gurney A.L.;

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY138965; AAN52117.1; -

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00409; IG; 2.

DR PROSITE; PSS0835; IG_LIKE; 2.

SQ SEQUENCE 394 AA; 44339 MW; 64B542F9384C7642 CRC64;

Query Match	100.0%;	Score 2067;	DB 4;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 3.1e-181;		
Matches 394;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFCPLKLLPVLDDYSLGLNDLVNVPPELTVHVGDSALMGCVFQSTEDKCIKFKIDWTLS	60	
Db	1	MFCPLKLLPVLDDYSLGLNDLVNVPPELTVHVGDSALMGCVFQSTEDKCIKFKIDWTLS	60	
QY	61	PGEHAKDEYLVLYYNNLSVPICRQNRVHLMGDIILCNDGSLLLQVQEAQDQTYICEIRL	120	
Db	61	PGEHAKDEYLVLYYNNLSVPICRQNRVHLMGDIILCNDGSLLLQVQEAQDQTYICEIRL	120	
QY	121	KGESOVFKKAVLVHVLPEPKELMHVHGLTMGCVFQSTEVKHVTKVWFIPSGRAKKE	180	
Db	121	KGESOVFKKAVLVHVLPEPKELMHVHGLTMGCVFQSTEVKHVTKVWFIPSGRAKKE	180	

QY	181	IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMQLGVRSDDGNYTCSIHLGN	240
Db	181	IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMQLGVRSDDGNYTCSIHLGN	240
QY	241	LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVLIIGVICATILLLPVLILIVKKT	300
Db	241	LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVLIIGVICATILLLPVLILIVKKT	300
QY	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIVREVIIEEPESEKSEAT	360
Db	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIVREVIIEEPESEKSEAT	360
QY	361	YMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF	394
Db	361	YMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF	394
RESULT 2			
ID	Q8N9I7	PRELIMINARY;	PRT; 384 AA.
AC	Q8N9I7	01-OCT-2002 (TREMBlrel. 22, Created)	
DT	01-OCT-2002	(TREMBlrel. 22, Last sequence update)	
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)	
DE	Hypothetical protein FLJ37080.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Cerebellum;		
RA	Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hiroo M., Shimizu F.,		
RA	Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,		
RA	Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,		
RA	Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,		
RA	Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,		
RA	Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,		
RA	Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,		
RA	Masuo Y., Nagai K., Isegai T.;		
RT	"NEDO human cDNA sequencing project";		
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AK094399; BAC04347.1; --		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	SMART; SMO0409; IG; 2.		
DR	PROSITE; PS50835; IG LIKE; 2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 384 AA; 43091 MW; C93D8EF6C97B6591 CRC64;		
Query Match			
Best Local Similarity 96.0%; Score 1985; DB 4; Length 384;			
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	15	DYSLGDLNVSPELTVHVGDSALMGCVFQSTEDKCIKIDWTLSPGEHAKDEVLVYY	74
Db	5	DYSLGDLNVSPELTVHVGDSALMGCVFQSTEDKCIKIDWTLSPGEHAKDEVLVYY	64
QY	75	SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQADQGTTCIEIRLKGESQVFKKAVVLH	134
Db	65	SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQADQGTTCIEIRLKGESQVFKKAVVLH	124
QY	135	VLPEPKELMHVGLLIOMGCVFQSTEVKHTVKEWIFSGRAKEEIVFRYHKLMSVE	194
Db	125	VLPEPKELMHVGLLIOMGCVFQSTEVKHTVKEWIFSGRAKEEIVFRYHKLMSVE	184
QY	195	YSQSWGHFQNRVNLVGDIFRNDGSLMQLGVRSDDGNYTCSIHLGN	254
Db	185	YSQSWGHFQNRVNLVGDIFRNDGSLMQLGVRSDDGNYTCSIHLGN	244
QY	255	EPRTLVTAPALRPLVLGGNQLVLIIGVICATILLLPVLILIVKKTGKSSVNSTVLVKN	314
RESULT 4			
Q8NF70			
Db	245	EPRTLVTAPALRPLVLGGNQLVLIIGVICATILLLPVLILIVKKTGKSSVNSTVLVKN	304
QY	315	TKTNPETKEKPKCHFERCEGEKHIYSPPIVREVIIEEPESEKSEATVMTMHPVWPSLRSD	374
Db	305	TKTNPETKEKPKCHFERCEGEKHIYSPPIVREVIIEEPESEKSEATVMTMHPVWPSLRSD	364
QY	375	RNNSLEKSGGMPKTOQAF	394
Db	365	RNNSLEKSGGMPKTOQAF	384
RESULT 3			
ID	Q7Z499	PRELIMINARY;	PRT; 394 AA.
AC	Q7Z499	01-OCT-2003 (TREMBlrel. 25, Created)	
DT	01-OCT-2003	(TREMBlrel. 25, Last sequence update)	
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)	
DE	Putative junctional adhesion molecule precursor.		
GN	JAML.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Bone marrow;		
RA	Moog-Lutz C., Cave-Riant F., Guibal F.C., Breau M., Di Gioia Y.,		
RA	Cayre Y.E., Lutz P.G.;		
RT	"JAML, a novel protein induced in myeloid leukemia cells, has		
RT	characteristics of a junctional adhesion molecule.";		
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ515553; CAD56620.1; --		
KW	Signal.		
FT	SIGNAL 1 19 Potential.		
FT	CHAIN 20 394 putative junctional adhesion molecule.		
SQ	SEQUENCE 394 AA; 43731 MW; B81F99C929D80C53 CRC64;		
Query Match			
Best Local Similarity 86.3%; Score 1783; DB 4; Length 394;			
Matches 354; Conservative 7; Mismatches 20; Indels 26; Gaps 4;			
QY	1	MFCPLKLILPVLDDYSLGDLNVSPELTVHVGDSALMGCVFQSTEDKCIKIDWTL	60
Db	1	MFCPLKLILPVLDDYSLGDLNVSPELTVHVGDSALMGCVFQSTEDKCIKIDWTL	60
QY	61	PGEHAKDEYLYYYNSLSPICRQNRVHLMGDILCNDGSLLLQDVQADQGTTCIEIRL	120
Db	61	PGEHAKDEYLYYYNSLSPICRQNRVHLMGDILCNDGSLLLQDVQADQGTTCIEIRL	120
QY	121	KGESQVFKKAVVLHVLPEEPKELMHVGLLIOMGCVFQSTEVKHTVKEWIFSGRAKEE	180
Db	121	KGESQVFKKAVVLHVLPEEPKELMHVGLLIOMGCVFQSTEVKHTVKEWIFSGRAKEE	168
QY	181	IVF-----RYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMQLGVRS	227
Db	169	LYFVTTTNSGCLRTPRAGATSRIGSE-TRDQGRMDIFVNLVGDIFRNDGSLMQLGVRS	227
QY	228	DGNYTCSIHLGNLVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVLIIGVICATIL	287
Db	228	DGNYTCSIHLGNLVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVLIIGVICATIL	287
QY	288	LLPVLILIVKKTGKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIVRE	347
Db	288	LLPVLILIVKKTGKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIVRE	347
QY	348	TEEPEPSKSEATVMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF	394
Db	348	TEEPEPSKSEATVMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF	394


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ID Q8NF70 PRELIMINARY; PRT; 283 AA.
AC Q8NF70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FLJ00300 protein (Fragment).
GN FLJ00300.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Spine;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RL spleen."
DR EMBL; AK090409; BAC03390.1; -
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG-like.
DR PROSITE; PS00835; IG-LIKE; 2.
FT NON TER
SQ SEQUENCE 283 AA; 32079 MW; CCACB5B0839BB30E CRC64;

Query Match 66.0%; Score 1364; DB 4; Length 283;
Best Local Similarity 99.2%; Pred. No. 7.3e-117;
Matches 257; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLVDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTL 60
DB 25 MFCPLKLLPVLVDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTL 84
QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGYICE 120
DB 85 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGYICE 144
QY 121 KGSQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEIFSGRAKEE 180
DB 145 KGSQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEIFSGRAKEE 204
QY 181 IVFRYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCIHLGN 240
DB 205 IVFRYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCIHLGN 264
QY 241 LVFKKTIIVHVSPEEPTL 259
DB 265 LVFKKTIIVHVSPEEPTL 283

RESULT 5
Q8OUL9
ID Q8OUL9 PRELIMINARY; PRT; 379 AA.
AC Q8OUL9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to adhesion molecule AMICA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=B5/EGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell;
RA Strausberg R.;
DR EMBL; BC050133; AAH50133.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.

Query Match 9.6%; Score 198; DB 13; Length 335;
Best Local Similarity 22.1%; Pred. No. 1.2e-09;
Matches 88; Conservative 74; Mismatches 158; Indels 78; Gaps 17;

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DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG-LIKE; 2.
SQ SEQUENCE 379 AA; 42561 MW; 2CC0F2987CB12B7F CRC64;

Query Match 47.5%; Score 982; DB 11; Length 379;
Best Local Similarity 56.1%; Pred. No. 1.3e-81;
Matches 222; Conservative 35; Mismatches 105; Indels 34; Gaps 9;

QY 1 MFCPLKLLPVLVDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDW 57
DB 1 MFCPLKLLPVLVDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDW 60
QY 58 TLPSEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGYICE 117
DB 61 LFSKDDKDDASEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGYICE 120
QY 118 IRLKGSQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEIFSGRR 176
DB 121 IRLKESVMWKKPVLELWVLPPEPKDLRVVGDITQMRCSIQSTBEKRVTKVNMWPFSSGSH 180
QY 177 AKBEIVFRYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCI 236
DB 181 TEEETVLSYDSNMRSG--KFQSLGRFRFRVLDLTGDISRNDGSIKLTWVKESDRGIYTCI 238
QY 237 HLGMLVFKKTIIVHVSPEEPTLIVTPAALRPL-----VLGGNOLVIVGVCATILLP 290
DB 239 YVGKLESRTIIVHVVQDEFQRTISPTP--PTDKGQGIILGNOLVIVGVCATILLP 296
QY 291 VLILIVKTKCNKSSVNTVLVK---NTKTNPEIKPKCHFERCEGEKHIYSPIIIVREV 347
DB 297 VLILIVKAKWKKSSVSSMASVKLENKEKINP-----EKHIYSSITTTWET 342
QY 348 IEEEFSEKSEAYMTMHPVWPSLRSDRNNLSLEKS 383
DB 343 TERGISGE-SEGTYMTMNPVWPS--SPKASSLVRSS 375

RESULT 6
Q9YGV5
ID Q9YGV5 PRELIMINARY; PRT; 335 AA.
AC Q9YGV5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cht1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RC MEDLINE=99077161; PubMed=9862345;
RA Chretien I., Marcuz A., Courtet M., Katevuo K., Vainio O., Heath J.K.,
RA White S.J., Du Pasquier L.;
RT "CTX, a Xenopus thymocyte receptor, defines a molecular family
RT conserved throughout vertebrates."
RL Eur. J. Immunol. 28:4094-4104(1998).
DR EMBL; AF061023; AADI7523.1; -
DR HSSP; P06907; 1NEU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
SQ SEQUENCE 335 AA; 36561 MW; 071A313C3CE6DCA0 CRC64;

Query Match 9.6%; Score 198; DB 13; Length 335;
Best Local Similarity 22.1%; Pred. No. 1.2e-09;
Matches 88; Conservative 74; Mismatches 158; Indels 78; Gaps 17;

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Db	60	FYSAKESQLHTIYYISGQSYSGYGFKDRI--TAATSPGNASITISNMQPSDTG	SYTCEV	117	
Qy	119	RL-----KGESQVFKAVLVHL--PEEP-----KELMVHVGGLIOMGCVFQSTEVKHVTKVE	169		
Db	118	FSPQDDAGOSQ---KSVIVNVLVKPSKPFCKIEGTPEKGLIYLLCKCDQ-GLP	PHPT---170		
Qy	170	WIFSGRAKEEIVFRYYHKLMSVYSQSMGHFQNRVNLVGDIFRNDGSI	MLQG-VRES	228	
Db	171	-----YRWY-----KVD-----ENTLTPVTEYFNP	DTGILYIGNLTTFE	204	
Qy	229	GGNYTCSIHGLNLFVKKTIVLHVSPEEPRTLVP	PAALRPLVLGGNQLVIVGIVCATILL	288	
Db	205	TGHYRCI--ASNIMGNSTCELDLTSMSHSDGNIVAGAL	-----IGAILAAVII	249	
Qy	289	LPVLLIIVKTCGNKSVNSTVLVKNTKTNPKEKPC	HPERCEGEGKHIYSPPIVREVI	348	
Db	250	CATVWLVTAKKKKSSNE-MQVMAQKQSN	AEYAQVP-----NEENTPATAVLPSNA	301	
Qy	349	EEEEPSEKSEATYMTMHPVMPSLRSDRNSLEK	KSGG	386	
Db	302	TNEQPSADEAAA-----PETP--ENDEKHEVQKE	ETAG	332	
RESULT 8					
Q9YGH1	PRELIMINARY; PRT; 335 AA.				
ID	AC	Q9YGH1			
DT	01-MAY-1999	(TREMBlrel. 10, Created)			
DT	01-MAY-1999	(TREMBlrel. 10, Last sequence update)			
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)			
DE	Chrl	thymocyte antigen precursor.			
GN	Chrl.				
OS	Gallus	gallus (Chicken).			
OC	Eukaryota	; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria	; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=RPRL line 0;	TISSUE=Thymus;			
RA	Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,				
RA	Vainio O.;				
RT	"Chrl, a new IgSF member inhibits thymocyte differentiation at the				
RT	double positive stage.;"				
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; Y14063; CAA74390.1; -.				
DR	HSSP; P06907; INEU.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; Igv_1.				
DR	PROSITE; PS50835; IG_LIKE; 2.				
KW	Signal.				
FT	SIGNAL	1 21	POTENTIAL.		
FT	CHAIN	22 335	CHTL THYMOCTE ANTIGEN.		
SQ	SEQUENCE	335 AA; 36553 MW; AA640C5CD02CB16D	CRC64;		
Query Match 9.2%; Score 191; DB 13; Length 335;					
Best Local Similarity 22.1%; Pred. No. 5.1e-09;					
Matches 88; Conservative 76; Mismatches 156; Indels 78; Gaps 18;					
Qy	1	MFCPLKLIILLPVLLDYSGLNDLNVSPPELT	VHV--GDSALMGCVFQSTEDKCI	FKIDWT	58
Db	1	MF-PTMLKIFPILATLAGHVRGVVTVPEKTVNVK	TGGNATLLCTYTSSQPLGNFFIOWS	59	
Qy	59	LSPGGEHAKDEYVLYYSNLSPVIGRQFNVRHLMG	DILNDGSLLLQDVQEOADQGT	YICEI	118
Db	60	FYSAKESQLHTIYYISGQSYSGYGFKDRI--TAATSPGNASITISNMQPSDTG	SYTCEV	117	
Qy	119	RL-----KGESQVFKAVLVHL--PEEP-----KELMVHVGGLIOMGCVFQSTEVKHVTKVE	169		
Db	118	FSPQDDAGOSQ---KSVIVNVLVKPSKPFCKIEGTPEKGLIYLLCKCDQ-GLP	PHPT---170		

1	MF	CPLKLIILLPVLLDYSGLNDLNVSPPELT	VHV--GDSALMGCVFQSTEDKCI	FKIDWT	58
1	MF	PTMLKIFPILATLAGHVRGVVTVPEKTVNVK	TGGNATLLCTYTSSQPLGNFFIOWS		59
59	LS	PGEHAKDEYVLYYSNLSPVIGRQFNVRHLMG	DILNDGSLLLQDVQEOADQGT	YICEI	118
60	FYS	AKESQLHTIYYISGQSYSGYGF	KDRI--TAATSPGNASITISNMQPSDTG	SYTCEV	117
119	RL	-----KGESQVFKAVLVHL--PEEP	-----KELMVHVGGLIOMGCVFQ	STEVKHVTKVE	169
118	FSP	QDDAGOSQ---KSVIVNVLVKPSKPFCKIE	GTPEKGLIYLLCKCDQ-GLS	HTP---	170
170	WIF	SGRAKEEIVFRYYHKLMSVEYSQSMGHFQNR	VNLVGDIFRNDGSI	MLQ--VRES	228
171	-----	YRWY-----KVD-----	ENTLTPVTEYFNP	DTGILYIGNLT	TFE 204
229	GGNY	TCISHLGNLVFKKTI	VLHVSPEEPTLVTPAALRPLV	LGNGQLVIVGIV	CATILL 288
205	TG	HYRCI--ASNINGNST	CELDLTSMSHSDGNIVAGAL	-----	IGAILAAVII 249
289	LPV	LILIVKTCGNKSVNSTVLVNTKKTNPKEKPC	HPERCEGEGKHI	YSPPIVREVI	348
250	CAI	VWLVTKAKKKSSNE-MQVMAQKQ	SNAEYAQVP-----	NEENTPQPAVL	PSNA 301
349	EEEE	PSKSEATYMTMHPVWPSLRSDRNSLEK	KSGG	386	
302	TNEQ	PSADEAAASETP-----	ENDEKHEVQKE	ETAG	332

RESULT 7

Q9PWR4

PRELIMINARY; PRT; 335 AA.

Q9PWR4;

01-MAY-2000 (TREMBlrel. 13, Created)

01-MAY-2000 (TREMBlrel. 13, Last sequence update)

01-OCT-2003 (TREMBlrel. 25, Last annotation update)

Chrl thymocyte antigen precursor.

Chrl.

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Gallus.

NCBI_TaxID=9031;

[1]

SEQUENCE FROM N.A.

STRAIN=H.B19; TISSUE=Thymus;

Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,

Vainio O.;

"Chrl, a new IgSF member inhibits thymocyte differentiation at the

double positive stage."

Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

EMBL; Y14064; CAA74391.1; -.

HSSP; P06907; INEU.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig_1.

SMART; SM00406; Igv_1.

PROSITE; PS50835; IG_LIKE; 2.

Signal.

SIGNAL.

1 21 POTENTIAL.

22 335 CHTL THYMOCTE ANTIGEN

SEQUENCE 335 AA; 36509 MW; AA6159598079B438 CRC64;

Query Match 9.3%; Score 192; DB 13; Length 335;

Best Local Similarity 22.1%; Pred. No. 4.1e-09;

Matches 88; Conservative 76; Mismatches 156; Indels 78; Gaps 18;

1	MF	CPLKLIILLPVLLDYSGLNDLNVSPPELT	VHV--GDSALMGCVFQSTEDKCI	FKIDWT	58
1	MF	PTMLKIFPILATLAGHVRGVVTVPEKTVNVK	TGGNATLLCTYTSSQPLGNFFIOWS		59
59	LS	PGEHAKDEYVLYYSNLSPVIGRQFNVRHLMG	DILNDGSLLLQDVQEOADQGT	YICEI	118

[illegible]

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QY 5 LKULILPVLIDYSLGUNDLNVSPELTVH--VGDSALMGCVFO-STEDKCIFKIDWLTSP 61
Db 5 LCFVLLLCGVVDFA--RSLJITTPPEEMIEKAKGETAVLPCKFTLSPDEQGLDIEWLISP 61
QY 62 GEBAKDEYLVLYXSNLSVPIGRF---QNRVHL-MGDLICNDGSLLOQDVOEADQGVICE 117
Db 62 ADNQKVDQVILYSGDKIVDDYYPDLKGRVHFTSNDLKSGDASINTNLQLSDIGTYQCK 121
QY 118 IRLKBSQVFKKAVLHLVLPPEPKELMHVGGLIOMGVF---QSTEVKHVTKVEMIFS 173
Db 122 V--KKAPGVANKIHLVVL-VKPSGARCVDGSEETGSDFKIKCEPKESGLPQYEW-- 175
QY 174 GRRAKEEIVFRYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSMLOGVRESDGNYT 233
Db 176 -----QKLSDSQKMTSN-----LAEMTSSV-----ISVKNASEYSGTVS 211
QY 234 CSTHLGNLVFKKTIIVLHVSPEBPRTLVTPAALRPLVLGNQVLVIIVGIVCATILLPLVLI 293
Db 212 CTVR--NRVGSQCLRLNWWPP-----SNKAGLIAGIIGTLLALALIG 254
QY 294 LIWKVTCGNKSSVNSVLVKNTKTNPEIKEXPCHPERCEGEKHIYSPILVREVTIEEPP 353
Db 255 LII-FCC-----RKKREEKYKEVHHD-----IREDVP 282
QY 354 SEKSEATYMTMHPVMPFSRESDRNN--SLEKSGGGGMPKTO 391

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Db 283 PPKSRTSTARS-IGSNHSSLGSMSPSNMEGYSKTQ 317

RESULT 11

Q9NR99 PRELIMINARY; PRT; 2828 AA.
AC Q9NR99;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Adlican.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta.
RA Crowl R.M., Luk D.;
RT "Identification of the gene encoding Adlican, a novel protein
RT expressed in human arthritic tissues."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF245505; AAF86402.1; -
DR HSP; P56276; 1TLK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00047; Ig; 12.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR SMART; SM00408; IGC2; 10.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 3.
DR PROSITE; PS00835; IG_LIKE; 12.
KW Immunoglobulin domain.
SQ SEQUENCE 2828 AA; 312291 MW; A18377D8554F1FE1 CRC64;

Query Match 8.1%; Score 167; DB 4; Length 2828;
Best Local Similarity 21.8%; Pred. No. 1.5e-05;
Matches 87; Conservative 74; Mismatches 149; Indels 90; Gaps 20;
QY 42 CVFQST--EDKCFKIDWTLSPG--EHAKD-EYVLYYSNL-----SVP 80
Db 2221 CVARNKVGDDYVVLKVDVVMKPAKIEHKENDHKVFYGGDLKVCVATCLPNPEISWSLP 2280
QY 81 IGRFQNRVHLMGD-----ILCNDGSLLODQVQADQGTIC--EIRL-KGESQVFK 129
Db 2281 DGLSNVSMQSDSGRTKRYVFNNGTLTFNEVGMBEGDYTCFAENQVGDENRVRVK 2340
QY 130 AVLHVLPEEPKELMVH--GGLIQMGCVFQTEVVKHVTKEWIFSGRRAKEEIVFRYYH 187
Db 2341 VTATPATENTKTYLAVQPYGDVTVAC---BAKGEPMKVTWLSPTNKV----- 2387
QY 188 KLRMSVEYSQSGHGFQNRVNLVGDIFRNDGSLMLQGVRESGDNCTCSHLGNLVFKKTI 247
Db 2388 -IPTSSEKQIY-----QDTLLIQAKRSDSGNVTCLVRNSAGEDRKVT 2431
QY 248 VLVHSPPEPRTLVTP---NALRPLVLGGNQLVI---IVGIVCATIL-LLPVLILVKKTC 300
Db 2432 WTHVNVQPPKINGNPNTITVREIAAGSGSRKILDCAKGIPTRVLWAPPEGVVLPAPY 2491
QY 301 GNKSSV--NSTVLVKNKTKTNPEIKPKCHFERCEGERKHYSPIIVREVEE---BEP-S 354
Db 2492 GNRITVHGNSLDIRLSKS--DSVQLVCMARNEGGEARLIIVQLTVLEPMKPIPHDPI 2549
QY 355 EKSEATYMTMHPV-----WPSLRSDRNNLSLEKSG 384
Db 2550 EK--ITAMAGHTISLNCSSAAGTPTPSLVVWLPNGTDLQSG 2587

RESULT 12

Q9TU80 PRELIMINARY; PRT; 319 AA.
AC Q9TU80;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE CoxSackie-adenovirus-receptor homolog (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed German shepherd; TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of CoxSackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109645; AAF01256.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
FT NON TR 319
SQ SEQUENCE 319 AA; 35422 MW; 85C63A6EC7986965 CRC64;

Query Match 7.9%; Score 164; DB 6; Length 319;
Best Local Similarity 22.6%; Pred. No. 1.4e-06;
Matches 91; Conservative 61; Mismatches 146; Indels 104; Gaps 19;
QY 5 LKLLPVLIDYSLGLNDLVNSPPELTVH--VGDSALMGCVFQ-STEDKCFKIDWTLSP 61
Db 5 LRFVLLCGVADFT---RSLSTTTPEQMLEKAKGETAYLPCKFTLSPEQGLDIEWLLSP 61
QY 62 GEHAKDEXVLYYYNSLVPIGRFQ--RVHL-MGDILCNDGSLLODQVQADQGTIC 117
Db 62 ADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKSGLDASINVTNRLSLDITYQCK 121
QY 118 IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVF---QSTEVKHVTKEWIF 173
Db 122 V--KKAQGVGNKKIQLTVL-VKPSGIRCYVDGSEIEGNDFKLKCPKESGLPQVW--- 175
QY 174 GRRAKEEIVFRYYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSLMLQGVRESGDNCT 233
Db 176 -----QKLSNSQKTPFSWS-----TDMTSPV-----ISIKNSTEYSGTYI 211
QY 234 CSHILGNLVFKKTIIVLHVSPE--EPTLVTPAARPLVLGGNQLVIIVGIVCATILLPV 291
Db 212 C-----TVTNRVGSDQCQLRLNVVPSNRAGTIAG---AVVG-----ILLALV 251
QY 292 LILIVKKTGCKNSSVNSVTLVKNTKTNPTEIKPKCHFERCEGERKHYSPIIVREVEE 351
Db 252 LIGFTVFC-----RKKRREEKYEKVVHHD-----IRE 280
QY 352 EPSEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGMPKQTQ 391
Db 281 VPLKSRSTARSY-----IGSNHSSLGSMSPSNMEGYSKTQ 317

RESULT 13

Q9H6B4 PRELIMINARY; PRT; 373 AA.
ID Q9H6B4
AC Q9H6B4;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 08:27:54 ; Search time 58 Seconds
(without alignments)
1919.374 Million cell updates/sec

Title: US-09-997-514-422

Perfect score: 2067

Sequence: 1 MFCPLKILLPVLLDYSGL.....RNSLEKSGGMPKTOQAP 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2067	100.0	394	3 AAY66764	Membrane-
2	2067	100.0	394	3 AAB33454	Aab33454 Human PRO
3	2067	100.0	394	3 AAY94452	Aay94452 Human inf
4	2067	100.0	394	3 AAB24433	Aab24433 Human PRO
5	2067	100.0	394	4 AAU12431	Aau12431 Human PRO
6	2067	100.0	394	4 AAM38860	Aam38860 Human pol
7	2067	100.0	394	4 AAB5287	Aab5287 Human PRO
8	2067	100.0	394	5 AAU83689	Aau83689 Human PRO
9	2067	100.0	394	5 ABB84933	Abb84933 Human PRO
10	2067	100.0	394	5 ABB95539	Abb95539 Human ang
11	2067	100.0	394	6 ABU58102	Abu58102 Human PRO
12	2067	100.0	394	6 ABU59180	Abu59180 Novel hum
13	2067	100.0	394	6 ABU82692	Abu82692 Human sec
14	2067	100.0	394	6 ABO17875	Abo17875 Novel hum
15	2067	100.0	394	6 ABU60611	Abu60611 Human sec
16	2067	100.0	394	6 ABU80836	Abu80836 Human PRO
17	2067	100.0	394	6 ABO33802	Abo33802 Novel hum
18	2067	100.0	394	6 ABU13993	Abu13993 Human PRO
19	2067	100.0	394	6 ABU81129	Abu81129 Human PRO
20	2067	100.0	394	6 ABU72578	Abu72578 Novel hum
21	2067	100.0	394	6 ABU66829	Abu66829 Human PRO
22	2067	100.0	394	6 ABU59910	Abu59910 Novel sec
23	2067	100.0	394	6 ABU59327	Abu59327 Human sec
24	2067	100.0	394	6 ABO26024	Abo26024 Human PRO
25	2067	100.0	394	6 ABO25100	Abo25100 Human sec

ALIGNMENTS

RESULT 1

AAY66764
ID AAY66764 standard; protein; 394 AA.

XX AAY66764;

XX AC

XX DT 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO1387.

XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX PN WO9963088-A2.

XX PD 09-DEC-1999. ✓

XX PF 02-JUN-1999; 99WO-US012252.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 03-JUN-1998; 98US-0087759P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088028P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 05-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

XX PR 05-JUN-1998; 98US-0088217P.

XX PR 09-JUN-1998; 98US-0088655P.

XX PR 10-JUN-1998; 98US-0088722P.

XX PR 10-JUN-1998; 98US-0088730P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088738P.

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XX PR 10-JUN-1998; 98US-0088742P.

XX PR 10-JUN-1998; 98US-0088810P.

XX PR 10-JUN-1998; 98US-0088811P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088825P.

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Abu59033 Human sec
Abu92411 Novel hum
Abu59476 Novel hum
Abu67105 Human sec
Abu92242 Novel hum
Abu10948 Human PRO
Abu81700 Novel hum
Abu88639 Human sec
Abo34153 Human PRO
Ada46039 Novel hum
Ada76470 Human PRO
Abj72325 Human PRO
Ada19120 Human PRO
Ada61743 Homo sapi
Adb19528 Novel hum
Adb28069 Human PRO
Ada86548 Novel hum
Adb16112 Human PRO
Ada37933 Human sec

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27 2067 100.0 394 6 ABU59033
28 2067 100.0 394 6 ABU92411
29 2067 100.0 394 6 ABU59476
30 2067 100.0 394 6 ABU67105
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32 2067 100.0 394 6 ABU10948
33 2067 100.0 394 6 ABU81700
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37 2067 100.0 394 6 ADA76470
38 2067 100.0 394 6 ABJ72325
39 2067 100.0 394 6 ADA19120
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42 2067 100.0 394 6 ADB28069
43 2067 100.0 394 6 ADA86548
44 2067 100.0 394 6 ADB16112
45 2067 100.0 394 6 ADA37933

PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
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PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
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PR 22-JUN-1998; 98US-0090246P.
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PR 01-JUL-1998; 98US-0091358P.
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PR 07-JUL-1998; 98US-0091982P.
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PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
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PR 10-AUG-1998; 98US-0095916P.

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PR 10-AUG-1998; 98US-0096012P.
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PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
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PR 20-AUG-1998; 98US-0097218P.
PR 20-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
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PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

(GETH) GENENTECH INC.

PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;

WPI; 2000-072883/06.

N-PSDB; AAZ65110.

Membrane-bound proteins and related nucleotide sequences.

Claim 12; Fig 304; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques

SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 3; Length 394;

Best Local Similarity 100.0%; Pred. No. 5.1e-188;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFCPLKLLPVLIDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60

Db 1 MFCPLKLLPVLIDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60

QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADOGTYICEIRL 120
 DB 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADOGTYICEIRL 120
 QY 121 KGESQVFKKAVLHVLPPEPKELMVHVGLIQMGCVFQSTEVKHVTKVEMIFSGRRAKEE 180
 DB 121 KGESQVFKKAVLHVLPPEPKELMVHVGLIQMGCVFQSTEVKHVTKVEMIFSGRRAKEE 180
 QY 181 IVFRIYHKLMSVYSOSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
 DB 181 IVFRIYHKLMSVYSOSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
 QY 241 LVFKKTTVLHVSPPEPTLVTPAALRPLVGLGNLVIIVGVICATILLLPVLLIVKTKC 300
 DB 241 LVFKKTTVLHVSPPEPTLVTPAALRPLVGLGNLVIIVGVICATILLLPVLLIVKTKC 300
 QY 301 GNKSSVNSTVLVKNKTKNPEIKPKCHFERCEGEKHIYSPIIIVREVIEEPEKSEAT 360
 DB 301 GNKSSVNSTVLVKNKTKNPEIKPKCHFERCEGEKHIYSPIIIVREVIEEPEKSEAT 360
 QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQA 394
 DB 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQA 394

RESULT 2
 AAB33454
 ID AAB33454 standard; protein; 394 AA.
 AC AAB33454;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PR01387 protein UNQ722 SEQ ID NO:187.
 XX
 KW Human; immune related disease; diagnosis; antinflammatory; cardiant;
 KW dermatologic; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200053758-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US005841.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 20-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99WO-US008615.
 PR 28-APR-1999; 99US-0131445P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX
 PA (GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 Kabakoff RC, Lau Y, Pan J, Pennica D, Shelton DL, Smith V;
 Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;

WPI; 2000-572271/53.

N-PSDB; AAC58619.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 82; 309pp; English.

The present invention describes sixty four human PRO proteins which can
 be used in the treatment of immune related diseases. The human PRO
 proteins, anti-PRO antibodies, agonists and antagonists are useful for
 treating and diagnosing immune related disorders. The disorders are
 selected from systemic lupus erythematosus, rheumatoid arthritis,
 osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 immune-mediated renal disease, demyelinating diseases of the central and
 peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 or immune-mediated skin diseases, allergic diseases, immunological
 diseases of the lung, and transplantation associated diseases including
 graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 represent PCR primers and hybridisation probes used in the isolation of
 human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 represent human PRO polynucleotide and protein sequences given in the
 exemplification of the present invention

Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 3; Length 394;
 Best Local Similarity 100.0%; Pred. No. 5.1e-188;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 DB 1 MFCPLKLLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADOGTYICEIRL 120

Db	61	PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDLNCDSGLLLQDVQVQADQGYTICIRL	120
Qy	121	KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVPQSTEVKHVTKEVIFSGRRAKEE	180
Db	121	KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVPQSTEVKHVTKEVIFSGRRAKEE	180
Qy	181	IVFRYHKLMSVEYSOSWGHFQNRVNLVGDIFRNDGSIHQVRESGNGNYTCSIHLGN	240
Db	181	IVFRYHKLMSVEYSOSWGHFQNRVNLVGDIFRNDGSIHQVRESGNGNYTCSIHLGN	240
Qy	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNQLVIVGIVCATILLPVLILIVKTC	300
Db	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNQLVIVGIVCATILLPVLILIVKTC	300
Qy	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVEEPEPEKSEAT	360
Db	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVEEPEPEKSEAT	360
Qy	361	YMTMHPVWPSPILSRDRNNSLEKKGSGGMPKTOQAF	394
Db	361	YMTMHPVWPSPILSRDRNNSLEKKGSGGMPKTOQAF	394
RESULT 3			
AA	AY94452		
ID	AA944452	standard; protein; 394 AA.	
AC	AA944452;		
XX	11-SEP-2000	(first entry)	
DT	Human inflammation associated protein #11.		
DE	Inflammation; rheumatoid arthritis; Crohn's disease; asthma;		
KW	multiple sclerosis; allergy; AIDS; diabetes mellitus antiinflammatory;		
KW	gene therapy; human.		
XX	Homo sapiens.		
XX	WO200029574-A2.		
XX	25-MAY-2000.		
XX	04-NOV-1999;	99WO-US026234.	
XX	18-NOV-1998;	98US-00195232.	
XX	(INCY-) INCYTE PHARM INC.		
PI	Walker MG, Volkmut W, Klingler TM;		
DR	WPI; 2000-387787/33.		
DR	N-PSDB; AAA27133.		
PT	New human inflammation-associated polypeptide useful for diagnosis,		
PT	prevention and treatment of inflammatory diseases comprises product of		
XX	gene coexpressed with e.g. CD16, L-selectin and IP-30.		
PS	Claim 4; Page 42-43; 43pp; English.		
CC	Eleven novel inflammation-associated genes have been identified in cDNA		
CC	libraries from various tissues. The genes were selected according to		
CC	their coexpression with the known inflammation genes, CD16, L-selectin,		
CC	Src-like adapter protein, IP-30, superoxide homoenzyme subunits, alpha-		
CC	1-antitrypsin, C1q-A, 5-lipoxygenase activating protein and SRC family		
CC	tyrosine kinase. The novel polynucleotides may be used in hybridization		
CC	assays to diagnose a disease or condition associated with altered		
CC	expression of the inflammation genes. Antibodies against the genes may be		
CC	useful in compositions for the diagnosis and treatment of such diseases		
CC	associated with inflammation including rheumatoid arthritis, Crohn's		
CC	disease, multiple sclerosis, AIDS, diabetes mellitus, asthma and allergy.		
CC	Additionally the polynucleotides of the invention may be used for gene		
CC	therapy. The present sequence is human inflammation associated protein		

CC	#11, derived from Incyte Clone 3507924		
XX	Sequence 394 AA;		
SQ	Query Match	100.0%;	Score 2067; DB 3; Length 394;
	Best Local Similarity	100.0%;	Pred. No. 5.1e-188;
	Matches 394; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	1	MFCEPLKILLLPVLLDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIFKIDWTLS	60
Db	1	MFCEPLKILLLPVLLDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIFKIDWTLS	60
Qy	61	PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDLNCDSGLLLQDVQVQADQGYTICIRL	120
Db	61	PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDLNCDSGLLLQDVQVQADQGYTICIRL	120
Qy	121	KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVPQSTEVKHVTKEVIFSGRRAKEE	180
Db	121	KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVPQSTEVKHVTKEVIFSGRRAKEE	180
Qy	181	IVFRYHKLMSVEYSOSWGHFQNRVNLVGDIFRNDGSIHQVRESGNGNYTCSIHLGN	240
Db	181	IVFRYHKLMSVEYSOSWGHFQNRVNLVGDIFRNDGSIHQVRESGNGNYTCSIHLGN	240
Qy	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNQLVIVGIVCATILLPVLILIVKTC	300
Db	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNQLVIVGIVCATILLPVLILIVKTC	300
Qy	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVEEPEPEKSEAT	360
Db	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVEEPEPEKSEAT	360
Qy	361	YMTMHPVWPSPILSRDRNNSLEKKGSGGMPKTOQAF	394
Db	361	YMTMHPVWPSPILSRDRNNSLEKKGSGGMPKTOQAF	394
RESULT 4			
AA	AB24433		
ID	AB24433	standard; protein; 394 AA.	
AC	AB24433;		
XX	07-NOV-2000	(first entry)	
DT	Human PRO1387 protein sequence SEQ ID NO:220.		
DE	Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;		
KW	diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;		
KW	angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;		
KW	cytostatic; gene therapy; vaccine.		
XX	Homo sapiens.		
XX	WO200032221-A2.		
XX	08-JUN-2000.		
PD	30-NOV-1999;	99WO-US028313.	
XX	01-DEC-1998;	98WO-US025108.	
XX	16-DEC-1998;	98US-0112850P.	
XX	12-JAN-1999;	99US-0115554P.	
XX	08-MAR-1999;	99WO-US005028.	
XX	12-MAR-1999;	99US-0123957P.	
XX	28-APR-1999;	99US-0131445P.	
XX	14-MAY-1999;	99US-0134287P.	
XX	02-JUN-1999;	99WO-US012252.	
XX	23-JUN-1999;	99US-0141037P.	
XX	20-JUL-1999;	99US-0144758P.	
XX	26-JUL-1999;	99US-0145698P.	
XX	01-SEP-1999;	99WO-US020111.	
XX	08-SEP-1999;	99WO-US020594.	

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PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2000-412154/35.
XX N-PSDB; AAA77683.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating disorders in mammals.
XX
XX Claim 72; Fig 92; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating disorders in mammals by
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
XX Sequence 394 AA;
SQ
Query Match 100.0%; Score 2067; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCLPLILPVLDDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
Db 1 MFCLPLILPVLDDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQEAQGTTCIHL 120
Db 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQEAQGTTCIHL 120
QY 121 KGESQVFKKAVLHVLPPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEIFSGRAKEE 180
Db 121 KGESQVFKKAVLHVLPPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEIFSGRAKEE 180
QY 181 IVFRYHKLMSVEYSQSWGHGFQNRVNLVGDIFRNDGSIIMLGVRSDGNGNYTCSHLGN 240
Db 181 IVFRYHKLMSVEYSQSWGHGFQNRVNLVGDIFRNDGSIIMLGVRSDGNGNYTCSHLGN 240
QY 241 LVFKKTIHLVHVSPEERTLVTAAALRPLVLGNQLVIIVGIVCATILLPVLILVKKTC 300
Db 241 LVFKKTIHLVHVSPEERTLVTAAALRPLVLGNQLVIIVGIVCATILLPVLILVKKTC 300
QY 301 GNKSSVNSTVLVNTKTNPEIKPCPFCEKHIYSPILVREVIEEESSEKSEAT 360
Db 301 GNKSSVNSTVLVNTKTNPEIKPCPFCEKHIYSPILVREVIEEESSEKSEAT 360
QY 361 YMTMHPVWPSLRDRNNSLEKSGGGMPTQQA 394
Db 361 YMTMHPVWPSLRDRNNSLEKSGGGMPTQQA 394
```

RESULT 5
AAU12431

```
ID XX AAU12431 standard; protein; 394 AA.
AC XX AAU12431;
XX XX
DT 24-OCT-2001 (first entry)
XX XX
DE Human PRO1387 polypeptide sequence.
XX XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX XX
OS Homo sapiens.
XX XX
PN WO200140466-A2.
XX XX
PD 07-JUN-2001.
XX XX
PP 01-DEC-2000; 2000WO-US032678.
XX XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 03-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen WB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-408281/43.
XX N-PSDB; AAS21503.
XX
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
```

PT breast, prostate, cervical.
XX Claim 12; Fig 520; 813pp; English.
PS
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VITA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELVHMGDIILCNDGSLLLQDVQADQGTVCIEIRL 120
Db 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELVHMGDIILCNDGSLLLQDVQADQGTVCIEIRL 60
QY 61 PGEHAKDEYLVLYYSNLSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVCIEIRL 120
Db 61 PGEHAKDEYLVLYYSNLSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVCIEIRL 120
QY 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVKVEWIFSGRRAKEE 180
Db 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVKVEWIFSGRRAKEE 180
QY 181 IVFRYYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRYYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGN 240
QY 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNQLVLIIVGVCAITILLPVLILIVKKT 300
Db 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNQLVLIIVGVCAITILLPVLILIVKKT 300
QY 301 GNKSSVNSTVLVNTKTNPEIKKPCPFCEGEKHIYSPIIVREVIEEPESEKSEAT 360
Db 301 GNKSSVNSTVLVNTKTNPEIKKPCPFCEGEKHIYSPIIVREVIEEPESEKSEAT 360
QY 361 YMTWHPVWPSLRSDRNLSLEKSGGMPKTOQAF 394
Db 361 YMTWHPVWPSLRSDRNLSLEKSGGMPKTOQAF 394

RESULT 6
AAM38860
ID AAM38860 standard; protein; 394 AA.
XX
AC AAM38860;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2005.
XX
KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amytrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX Homo sapiens.
OS
XX WO200153312-A1.
PN
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000WO-US034263.
PF
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSR-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AAI58016.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PT
XX
PS Example 3; SEQ ID NO 2005; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nontropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELVHMGDIILCNDGSLLLQDVQADQGTVCIEIRL 60
Db 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELVHMGDIILCNDGSLLLQDVQADQGTVCIEIRL 60
QY 61 PGEHAKDEYLVLYYSNLSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVCIEIRL 120
Db 61 PGEHAKDEYLVLYYSNLSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVCIEIRL 120
QY 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVKVEWIFSGRRAKEE 180
Db 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVKVEWIFSGRRAKEE 180
QY 181 IVFRYYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRYYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGN 240

QY 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNOLVIIVGIVCATILLPVLILIVKTC 300
 DB 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNOLVIIVGIVCATILLPVLILIVKTC 300
 QY 301 GNKSSVNSTVLVKNKTINPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 DB 301 GNKSSVNSTVLVKNKTINPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394
 DB 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394

RESULT 7
 AAB65287
 ID AAB65287 standard; protein; 394 AA.
 AC AAB65287;
 XX
 DT 02-APR-2001 (first entry)
 XX Human PRO1387 (UNQ722) protein sequence SEQ ID NO:422.
 DE Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
 KW cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 XX 07-DEC-2000.
 XX
 XX 30-MAR-2000; 2000WO-US008439.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kijavain IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.
 DR N-PSDB; AAF44256.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target bioactive

PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX Claim 12; Fig 304; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
 Best Local Similarity 100.0%; Pred. No. 5.1e-188;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLDDYSLGDLNVPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 DB 1 MFCPLKLLPVLDDYSLGDLNVPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 QY 61 PGEHAKDEYVLYYYNSLVSPIGRPNRVHLMGDLICNDGSLLLQDVQADQGTVCIRL 120
 DB 61 PGEHAKDEYVLYYYNSLVSPIGRPNRVHLMGDLICNDGSLLLQDVQADQGTVCIRL 120
 QY 121 KGESQVFKKAVLHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTVKVEWIFSGRAKEE 180
 DB 121 KGESQVFKKAVLHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTVKVEWIFSGRAKEE 180
 QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 240
 DB 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 240
 QY 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNOLVIIVGIVCATILLPVLILIVKTC 300
 DB 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNOLVIIVGIVCATILLPVLILIVKTC 300
 QY 301 GNKSSVNSTVLVKNKTINPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 DB 301 GNKSSVNSTVLVKNKTINPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394
 DB 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394

RESULT 8
 AAU83689
 ID AAU83689 standard; protein; 394 AA.
 XX
 AC AAU83689;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 196.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.


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PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
XX N-PSDB; ABL88188.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 234; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal. e.g.
XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The PRO polynucleotides have applications in molecular biology,
XX including use as hybridisation probes, and in chromosome and gene
XX mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX exemplification of the present invention
XX
XX Sequence 394 AA;
XX
XX Query Match 100.0%; Score 2067; DB 5; Length 394;
XX Best Local Similarity 100.0%; Pred. No. 5, 1e-188;
XX Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MFCPLKLILLPVLLDYSGLNDLNVSPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKLILLPVLLDYSGLNDLNVSPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEYLYXXSNLSVPIGRFQNRVHLWGDIILNDGSLILLQDVQEQDGYICEIRL 120
Db 61 PGEHAKDEYLYXXSNLSVPIGRFQNRVHLWGDIILNDGSLILLQDVQEQDGYICEIRL 120
QY 121 KGSQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEMIFSGRRAKEE 180
Db 121 KGSQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEMIFSGRRAKEE 180
QY 181 IVFRYHKLMSVEYSQSGWHGFQNRVNLVGDIFRNDGSIIMLQGVRESDDGNYTCSIHGN 240
Db 181 IVFRYHKLMSVEYSQSGWHGFQNRVNLVGDIFRNDGSIIMLQGVRESDDGNYTCSIHGN 240
QY 241 LVFKKTLVHVSPEEPTLVTTPAALRPLVLGNGNLVIVGIVCATILLPVLILVKKTC 300
Db 241 LVFKKTLVHVSPEEPTLVTTPAALRPLVLGNGNLVIVGIVCATILLPVLILVKKTC 300
QY 301 GNKSVNSTVLVKNTKTNPEIKPCHFERCEGEKHIYSPPIIVREVIEEPESEKSEAT 360

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Db 301 GNKSVNSTVLVKNTKTNPEIKPCHFERCEGEKHIYSPPIIVREVIEEPESEKSEAT 360
QY 361 YMTMHPVPSLRSRDNNSLEKSGGGMPKTQOAF 394
Db 361 YMTMHPVPSLRSRDNNSLEKSGGGMPKTQOAF 394
RESULT 10
ABB95539
ID ABB95539 standard; protein; 394 AA.
XX
XX ABB95539;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human angiogenesis related protein PRO1387 SEQ ID NO: 234.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021735.
XX
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709338.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 22-JAN-2001; 2001US-00767609.
XX 28-FEB-2001; 2001US-00796498.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 09-MAR-2001; 2001US-00802706.
XX 14-MAR-2001; 2001US-00808689.
XX 22-MAR-2001; 2001US-00816744.
XX 05-APR-2001; 2001US-00828366.
XX 10-MAY-2001; 2001US-00854208.
XX 25-MAY-2001; 2001US-00866028.
XX 25-MAY-2001; 2001US-00866034.
XX 30-MAY-2001; 2001WO-US017092.
XX 30-MAY-2001; 2001US-00870574.
XX 01-JUN-2001; 2001WO-US017443.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX
XX (GETH ) GENENTECH INC.
XX (BAKE/) BAKER K P.
XX (FERR/) FERRARA N.
XX (GERB/) GERBER H.
XX (GERR/) GERRITSEN M E.
XX (GODD/) GODDARD A.
XX (GODO/) GODOWSKI P J.

```

PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAONI/) PAONI N P.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95677.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 234; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCEPLKILLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
Db 1 MFCEPLKILLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60

QY 61 PGHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGYICEIRL 120
Db 61 PGHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGYICEIRL 120

QY 121 KGSQVEKKAIVLHVLPEEPKELMVHVGGLIOMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180
Db 121 KGSQVEKKAIVLHVLPEEPKELMVHVGGLIOMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180

QY 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCSIHLGN 240
Db 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCSIHLGN 240

QY 241 LVFKKTIIVLHVSPEEPRTLTPAALRPLVIGGNOLVIVGIVCATILLLPVLILIVKTC 300
Db 241 LVFKKTIIVLHVSPEEPRTLTPAALRPLVIGGNOLVIVGIVCATILLLPVLILIVKTC 300

QY 301 GNKSSVNSTVLVNTKTNPEIKKPCHEKPCERCEKHIYSPITVREVIEEPESEKSEAT 360
Db 301 GNKSSVNSTVLVNTKTNPEIKKPCHEKPCERCEKHIYSPITVREVIEEPESEKSEAT 360

QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQAQ 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQAQ 394

RESULT 11
ABU58102
ID ABU58102 standard; protein; 394 AA.
XX
AC ABU58102;
XX

DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #134.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
XX US2003027163-A1.
XX
PD 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
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PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
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PR 04-JUN-1998; 98US-0088326P.
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PR 05-JUN-1998; 98US-0088212P.
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PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088714P.
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PR 19-JUN-1998; 98US-0089947P.
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PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.


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PR 23-JUN-1998; 98US-00903355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
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PR 25-JUN-1998; 98US-0090676P.
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PR 25-JUN-1998; 98US-0090694P.
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PR 25-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
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PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
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PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
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PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 23-AUG-1998; 98US-00980355P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006684.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5,1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFCEPLKLLPVLDDYSLGNDLNVSPPELTVHVGSALMGCVFQSTEDKCIKIDWTLS 60
Db 1 MFCEPLKLLPVLDDYSLGNDLNVSPPELTVHVGSALMGCVFQSTEDKCIKIDWTLS 60
Qy 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDLICNDGSLLLQDYOEADOGTYICEIRL 120
Db 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDLICNDGSLLLQDYOEADOGTYICEIRL 120
Qy 121 KGESQVFKKAVLHVLPEEPKELMHVVGGLIOMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
Db 121 KGESQVFKKAVLHVLPEEPKELMHVVGGLIOMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
Qy 181 IVERYTHKLRMSVEYSQSGWHGFQNRVNLVGDIFRNDGSIIMLQGVRESDDGNYTCSIHLGN 240
Db 181 IVERYTHKLRMSVEYSQSGWHGFQNRVNLVGDIFRNDGSIIMLQGVRESDDGNYTCSIHLGN 240
Qy 241 LVEKKTIVLHVSPEEPRTVTPAALRPVLGNGOLVLIIVGVCATILLPVLILVKKTC 300
Db 241 LVEKKTIVLHVSPEEPRTVTPAALRPVLGNGOLVLIIVGVCATILLPVLILVKKTC 300
```

Db 241 LVFKKTVLVHVSPEEPRTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLILIVKTC 300
Qy 301 GNKSSVNSTVLVMTKTNPEIKKPKCHPERCEBCKHIYSPIIVREVIEEPEKSEAT 360
Db 301 GNKSSVNSTVLVMTKTNPEIKKPKCHPERCEBCKHIYSPIIVREVIEEPEKSEAT 360
Qy 361 YMTWHPVWPSLRSDRNSLEKKGSGMPKTOQAF 394
Db 361 YMTWHPVWPSLRSDRNSLEKKGSGMPKTOQAF 394

RESULT 12
ABUS9180
ID ABUS9180 standard; protein; 394 AA.
XX AC ABUS9180;
XX DT 28-APR-2003 (first entry)
XX DE Novel human secreted or transmembrane protein PRO1387.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX OS Homo sapiens.
XX XX
PN US2002132252-A1.
PD 19-SEP-2002.
XX PF 14-NOV-2001; 2001US-00990442.
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075943P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 03-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.

10-JUN-1998; 98US-0088826P.
11-JUN-1998; 98US-0088858P.
11-JUN-1998; 98US-0088861P.
12-JUN-1998; 98US-0088876P.
16-JUN-1998; 98US-0089105P.
16-JUN-1998; 98US-0089440P.
16-JUN-1998; 98US-0089512P.
16-JUN-1998; 98US-0089514P.
17-JUN-1998; 98US-0089532P.
17-JUN-1998; 98US-0089538P.
17-JUN-1998; 98US-0089598P.
17-JUN-1998; 98US-0089599P.
17-JUN-1998; 98US-0089600P.
17-JUN-1998; 98US-0089653P.
18-JUN-1998; 98US-0089801P.
18-JUN-1998; 98US-0089907P.
18-JUN-1998; 98US-0089908P.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
07-OCT-1998; 98WO-US021141.
01-DEC-1998; 98WO-US025108.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
02-JUN-1999; 99WO-US012252.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
06-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.
(GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Gramaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Faoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2003-247083/24.
XX N-PSDB; AEX80392.
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346

PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.

XX Claim 12; Fig 304; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein

XX Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLS 60
DB 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLS 60
QY 61 PGHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGTVCIRL 120
DB 61 PGHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGTVCIRL 120
QY 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTVKEWIFSGRAKEE 180
DB 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTVKEWIFSGRAKEE 180
QY 181 IVFRYHKLMSVEYSQSWGHQFNRLVGDIFRNDGSIIMLGVRSDGNGNYTCSIHLGN 240
DB 181 IVFRYHKLMSVEYSQSWGHQFNRLVGDIFRNDGSIIMLGVRSDGNGNYTCSIHLGN 240
QY 241 LVFKKTIIVHVSPEEPRTVTPAALRPLVIGNQLVIVGIVCATILLPVLILVKKTC 300
DB 241 LVFKKTIIVHVSPEEPRTVTPAALRPLVIGNQLVIVGIVCATILLPVLILVKKTC 300
QY 301 GNKSSVNSTVLVNTKTNPEIKKCHPERCEGEKHIYSPILVREVIEEPEEPESEKSEAT 360
DB 301 GNKSSVNSTVLVNTKTNPEIKKCHPERCEGEKHIYSPILVREVIEEPEEPESEKSEAT 360
QY 361 YMTMHPVWPSLRDRNNSLEKSGGGMPTQQAF 394
DB 361 YMTMHPVWPSLRDRNNSLEKSGGGMPTQQAF 394

RESULT 13
ABU82692

ID ABU82692 standard; protein; 394 AA.
XX AC ABU82692;
XX DT 26-JUN-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO1387.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosa; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX OS Homo sapiens.
XX PN US2003032023-A1.
XX PD 13-FEB-2003.
XX PF 14-NOV-2001; 2001US-00990711.
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 05-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341980/32.
DR DR N-PSDB; ACD24112.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
XX Claim 12; Fig 520; 660pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFCPLKLLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKICFKIDWTLS 60
Db 1 MFCPLKLLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKICFKIDWTLS 60
Qy 61 PGEHAKDEYLVYYSNLSVPVIGRFQNRVHLMGDIICNDGSLLLQDVQADQGYICEIRL 120
Db 61 PGEHAKDEYLVYYSNLSVPVIGRFQNRVHLMGDIICNDGSLLLQDVQADQGYICEIRL 120
Qy 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLTQMGCVFQSTEVKHKVTKVWIFSGRAKEE 180
Db 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLTQMGCVFQSTEVKHKVTKVWIFSGRAKEE 180
Qy 181 IVFRYHKLRSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVESDGNVYCSIHGN 240
Db 181 IVFRYHKLRSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVESDGNVYCSIHGN 240
Qy 241 LVFKKTIIVHVSPEEPRTLVTAAALRPLVLGNQLVLIIVGIVCATILLPVLILIVKTC 300
Db 241 LVFKKTIIVHVSPEEPRTLVTAAALRPLVLGNQLVLIIVGIVCATILLPVLILIVKTC 300
Qy 301 GNKSSVNTVLVKNKTKNPETKEKPCPERCEGKHLYSPVIVREVIEEPESEKSEAT 360
Db 301 GNKSSVNTVLVKNKTKNPETKEKPCPERCEGKHLYSPVIVREVIEEPESEKSEAT 360
Qy 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF 394

RESULT 15

ABU60611
ID ABU60611 standard; protein; 394 AA.
XX AC ABU60611;
XX DT 01-MAY-2003 (first entry)
XX DE Human secreted/transmembrane protein, #170.
XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
XX KW diagnostic; therapeutic; gene therapy.
XX OS Homo sapiens.
XX PN US2002160384-A1.
XX PD 31-OCT-2002.
XX PF 14-NOV-2001; 2001US-00992598.
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.

PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US0005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US021547.
PR 01-DEC-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US028634.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US007377.
PR 02-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX XX

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Deanoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Kijavini IO, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;

XX WPI; 2003-288106/28.
XX N-PSDB; ABX90370.

XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes.

XX Claim 12; Fig 304; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX comprising a sequence without signal peptide and the nucleic acid
XX encoding them. The polypeptides can be used to raise antibodies that
XX specifically bind to the PRO polypeptide, for linking a bioactive
XX molecule to a cell expressing a PRO protein and for modulating at least
XX one biological activity of a cell. The PRO polypeptides or
XX polynucleotides are also useful in gene therapy, in chromosome
XX identification, as chromosome markers, or in generating probes. The PRO
XX polypeptides are useful as molecular markers for protein electrophoresis,
XX and the isolated nucleic acids may be used for recombinantly expressing
XX those markers. The PRO polypeptides and nucleic acids may also be used in
XX tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
XX PRO, and in affinity purification of PRO from recombinant cell culture or
XX natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
XX polynucleotides of the invention. Note: The sequence data for this patent

CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLDDYSLGDLNVPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
DB 1 MFCPLKLLPVLDDYSLGDLNVPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
QY 61 PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDLNVDGSLLLQDVQVQGVICIRL 120
DB 61 PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDLNVDGSLLLQDVQVQGVICIRL 120
QY 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
DB 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSGWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 240
DB 181 IVFRYYHKLMSVEYSQSGWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 240
QY 241 LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLPVLILIVKTC 300
DB 241 LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLPVLILIVKTC 300
QY 301 GNKSSVNSTVLVNTKTNPEIKEKPCFRCERKEKHYSPIIIVREVIEEPESEKSEAT 360
DB 301 GNKSSVNSTVLVNTKTNPEIKEKPCFRCERKEKHYSPIIIVREVIEEPESEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQAF 394
DB 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQAF 394

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Job time : 61 secs

